STIC-Biotech/ChemLib

STIC-Biotech/ChemL	.ID	179748		
From: Sent: To: Subject:	Ramirez, Delia Thursday, Decembe STIC-Biotech/Chem 10/602219	er 22, 2005 4:38 PM ILib		
Hi,				and the second s
I would like to request the f	ollowing searches:			
1. SEQ ID NO: 11 and 12 2. SEQ ID NO:12 in the pr		tabases (commercial and intermercial and intermercial and interference)	terference)	
Thank you very much,				
Delia M. Ramirez, Ph.D. Patent Examiner Recombinant Enzymes-Art Unit USPTO 400 Dulany Street, Remsen Bldg Alexandria, VA 22314 (571) 272-0938 delia.ramirez@uspto.gov		·		
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				DE0.22 N
Searcher:		******** Type of Search NA# AA#: S/L: Oligomer: Encode/Transl: Structure #: Text: Inventor: Litigation:		************* Vendors and cost where applicable STN: DIALOG: QUESTEL/ORBIT: LEXIS/NEXIS: SEQUENCE SYSTEM: WWW/Internet: Other (Specify):

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Sequence 19, Appl
Sequence 1001, Ap
Sequence 49, Appl
Sequence 47, Appl
Sequence 46, Appl
Sequence 45, Appl
Sequence 41, Appl
Sequence 25, Appl
 Sequence 9, Appli
Sequence 5, Appli
Sequence 18, Appli
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Sequence 21, P
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Patent No. 6887696;
GENERAL INFORMATION:
APPLICANT: GARGER, Stephen A.;
APPLICANT: TURREN, Thomas H.;
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION; FILE REFERENCE: 008010087CPUS06; CURRENT APPLICATION NUMBER: US/09/993,059; CURRENT PILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
SOSTWARE: FRASESQ for Windows Version 4.0
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ORGANISM: Homo sapiens
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    SEQ ID NO 11
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-MODEL=frame+ pin.model -DEV=xlp
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-G=/cgn2_1/USPTO_spool_p/US10602219/runat_23122005_151142_17165/app_query.fasta_1.583
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Sequence 11, Appl
                                                                                              December 26, 2005, 10:52:16; Search time 233 Seconds (without alignments) 3211.817 Million cell updates/sec
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1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

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5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*

7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*

8: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RB_COMB.seq:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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FEATURE:

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LOCATION: (1)...(1275)

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Pred. No.:
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Percent Similarity: 1
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Query Match: 3
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                                                                                                      GACTGGGGGAGTAGATCTGCTAAAATTTGATGGTTGTTACTGTGACAGTTTGGAAAATTTG
                                                                                                                             AlaAapGlyTyrLysHisMetSerLeuAlaLeuAsnArgThrGlyArgSerIleValTyr
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US-09-993-059-7
; Sequence 7, Application US/09993059
; Patent No. 6887566
; GENERAL INPORMATION:
; APPLICANT: GARGER, Stephen A.
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221 GlnTyrCysAsnHisTrpArgAsnPheAlaAspIleAspAspSerTrpLysSerIleLys 240
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APPLICANT: TURPEN, Thomas H.
APPLICANT: KUMAGAI, Monto H.
TITLE OF INVENTION: FRODUCTION OF LYSOSOMAL ENZYMES IN
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
FILE REFERENCE: 008010087CPUS06
CURRENT APPLICATION NUMBER: US/09/993,059
CURRENT FILING DATE: 201-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 1278
TYPE: DNA
TYPE: DNA
CORGANISM: Homo sapiens
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Matches:
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Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 3 Gaps: 0 US-10-602-219-12 (1-421) x US-10-103-327-7 (1-1278)	1 MetGlnLeuargaanProGluLeuHisLeuGlyCy 	Qy 21 LeuValSerTrpAspIleProGlyAlaArgAlaLeuAspAsnGlyLeuAlaArgThrPro 40		Oy 61 AspSerCyslleSerGluLysLeuPheMetGluMetAlaGluLeuMetValSerGluGly 80	Qy 81 TrpLysAspAlaGlyTyrGluTyrLeuCysIleAspAspCysTrpMetAlaProGlnArg 100	Qy 101 AspSerGluGlyArgLeuGlnAlaAspProGlnArgPheProHisGlyIleArgGlnLeu 120	Qy 121 AlaasnTyrValHisSerLysGlyLeuLysLeuGlyIleTyrAlaaspValGlyAsnLys 140	Qy 141 ThrCysAlaGlyPheProGlySerPheGlyTyrTyrAsp1leAspAlaGlnThrPheAla 160	Qy 161 AspTrpGlyValAspLeuLeuLysPheAspGlyCysTyrCysAspSerLeuGluAsnLeu 180	Qy 181 AlaAspGlyTyrLysHisMetSerLeuAlaLeuAsnArgThrGlyArgSerIleValTyr 200	Oy 201 SerCysGluTrpProLeuTyrMetTrpProPheGlnLysProAsnTyrThrGluIleArg 220	Oy 221 GlnfyrCysAsnHisTrpArgAsnPheAlaAsplleAspAspSerTrpLysSerIleLys 240 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 241 SerIleLeuAspTrpThrSerPheAsnGlnGluArgIleValAspValAlaGlyProGly 260	Qy 261 GlyTrpAsnAspProAspMetLeuVallleGlyAsnPheGlyLeuSerTrpAsnGlnGln 280	Qy 281 ValThrGlnWetalaLeuTrpAlaileMetalaAlaProLeuPheWetSerAsnAspLeu 300	Qy 301 ArgHisIleSerProglnAlaLysAlaLeuLeuGlnAspLysAspVall1eAla1leAsn 320	Qy 321 GlnAspProLeuGlyLysGlnGlyTyrGlnLeuArgGlnGlyAspAsnPheGluValTrp 340 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
	721 AGTATCTTGGACTGGACATCTTTTAACCAGGAGAGAATTGTTGATGTTGCTGGACCAGGG 261 GlyTrpAsnAspProAspMetLeuVallleGlyAsnPheGlyLeuSerTrpAsnGlnGln	DD 781 GGTTGGAATGACCCAGATATGTTGGCATTTGGCAACTTTGGCCTCAGCTGGAATCAGCAA 840 Qy 281 ValThrGlnMetAlaLeuTrpAlaIleMetAlaAlaProLeuPheMetSerAsnAspLeu 300 Dh 641 GTAAACTCAGAAACCCCAGAAAAAAAAAAAAAAAAAAAA	301 ArgHislleSerProGlnAlalysAlaLeuLeuGlnAspLysAspVallleAlalleAss 3	321 GlnaspProLeuGlyLysGlnGlyTyrGlnLeuArgGlnGlyAspAsnPheGluValTrp 3	341 GluargProLeuSerGlyLeuAlaTrpAlaValAlaWetIleAsnArgGlnGluIleGly [361 GlyProArgSerTyrThrileAlaValAlaSerLeuGlyLysGlyValAlaCysAsnPro 3 [381 AlaCysPhelleThrGhiceLeuLeuProValLysArgLysLeuGlyPheTyrGluTrpThr	401 SerArgLeuArgSerHisIleAsnProThrGlyThrValLeuLeuGlnLeuGluAsnThr 4	1201 TCAAGGTTAAGAAGTCACATAAATCCCACAGGCACTGTTTTGCTTCAGCT	DD 1261 ATG 1263 RESULT 4 US-10-103-327-7	; Sequence 7, Application US/10103327 ; Patent No. 6890748 ; GENERAL INFORMATION: ; APPLICANT: GARGER, Stephen A.	; APPLICANT: TURPEN, Thomas H.; ; TAPLICANT: KUMAGAI, MONCO H. ; TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN ; TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION	; FILE KEFERENCE: U08010087CPUSO6; CULE KEFERENCE: U08010087CPUSO6; CURRENT APPLICATION NUMBER: U5/10/103,327; CURRENT FILING DATE: 2002-03-20; PRIOR APPLICATION NUMBER: U5/09/993,059	0,	LENGTH: 1278 ; TYPE: DNA ; ORGANISM: Homo sapiens ; FEATURE:		Alignment Scores: 8.19e-252 Length: 1278 Pred. No.: 2314.00 Matches: 421 Score: 2314.00 Matches: 421 , Percent Similarity: 100.00% Conservative: 0

Db 241 TGGAAGGATGCAGGTTATGAGTACCTCTGCATTGATGATGGCTCCCCAAAGA 300	Oy 161 ABPTrpGlyValAspLeuLyBPheAspGlyCysTyrCysAspSerLeuGluAsnLeu 180	SerCygGluTrpProLeuTyrMetTrpProPheGlnLysProAsnTyrThrGlu11eArg	Qy 241 SerileLeuAspTrpThrSerPheAsnGlnGluAry11eValAspValAlaGlyProGly 260		GluargProLeuSerGlyLeualaTrpalaValalaMetileasnArgGlnGluileGly		Oy 421 Met 421
341 GluargProLeuSerGlyLeualaTrpalavalalametileasnargGlnGluileGly 36	Qy 401 SerArgleaArgSerHi011EARDFrGhrGlyThrValleauLeuGluAenThr 420 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	RESULT 5 US-09-993-059-13 i Sequence 13, Application US/09993059 j Batent No. 6887696 j GENERAL INFORMATION: APPLICANT: GARGER, Stephen A. APPLICANT: TURPEN, Thomas H. APPLICANT: TURPEN, THOMAS H. ITITLE OF INVENTION: PRODUCTION OF LYSOSOWAL ENZYMES IN	CON: PLANTS BY TRANSIENT EXPRESSION 008010087CPUS06 IION NUMBER: US/09/993,059 ATE: 2001-11-13 NOS: 37 CO for Windows Version 4.0	iens 284) 8.25e-252 Length: 2314.00 Matches: 100.00% Conservative:	-993-05 GluLeuH 	21 LeuvalSerTrpaspileProGlyalaArgAlaLeuAspasnGlyLeuAlaArgThrPro 4 [61 AspSerCyslleSerGluLysLeuPheMetGluMethlaGluLeuMetValSerGluGly

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US-09-993-059-3

Sequence 3, Application US/09993059

Sequence 3, Application US/09993059

Patent No. 6887696

GENERAL INFORMATION:

APPLICANT: GARGER, Stephen A.

APPLICANT: TURPEN, THOMASH.

APPLICANT: TURPEN, THOMASH.

TITLE OF INVENTION: PRODUCTION OF LYSOSOWAL ENZYMES IN

TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION

TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION

TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION

CURRENT APPLICATION NUMBER: US/09/993,059

CURRENT APPLICATION NUMBER: US/09/993,059

CURRENT APPLICATION NUMBER: US/09/993,059

CURRENT ELING DATE: 2001-11-13

NUMBER OF SEQ ID NOS: 37

SEQ ID NO 3

LENGTHAR: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 1290
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: GARGER, Stephen A.
APPLICANT: TURPER, Thomas H.
APPLICANT: TURPEN, Thomas H.
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
TITLE OF INVENTION: PLANTS BY 1001.00970.0000
CURRENT FILING DATE: 2000.00970.0000
PRIOR APPLICATION NUMBER: US/09/993,059
PRIOR PILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 1284
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Matches:
Conservative:
Mismatches:
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Gaps:
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2314.00
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CRGANISM: Homo sapiens
FRATURE:
NAME/KEY: CDS
LOCATION: (1)...(1284)
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Best Local Similarity:
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321 GlnAspProLeuGlyLysGlnGlyTyrGlnLeuArgGlnGlyAspAsnPheGluValTrp	Qy 381 AlaCysPhelleThrGluLeuLeuLeuLysArgLysHerVEUUTPIThr 400	Oy 421 Met 421	្រួលល	; APPLICANT: KUMAGAI, MONICO H. ; TITLE OF INVENTION: PRODUCTION OF LYSOSOWAL ENZYMES IN ; TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION ; FILE REFERENCE: 008010087CPUSO6 ; CURRENT APPLICATION NUMBER: US/10/103,327	CURRENT FILING DATE: 2002-03-20 PRIOR APPLICATION NUMBER: US/09/993,059 PRIOR FILING DATE: 2001-11-13 NUMBER OF SEQ ID NOS: 37	; SCFTWARE: FASESEQ IOF WINDOWS VERION *.0 ; LENGTH: 1290 ; TYPE: DNA	CASATURE	res: 8.31e-252 Length: 2314.00 Matches:	<pre>it Similarity: 100.00\$.ocal Similarity: 100.00\$ Match:</pre>	-10-602-219-12 (1-421) x US-10-103-327-3 (1-1290)	1 MetGlnLeuarghanProGluLeudisLeudisLycyaalaleualaleuargPneLeudia 	LeuvalSetTrpAspIleProGlyAlaArgAlaLeubspAsnGlyLeuAlaArgThrPro 		Qy 61 AspSerCysIleSerGluLysLeuPheMetGluMetAlaGluLeuMetValSerGluGly 80
Pred. No.: Score: 2314.00 Matches: 1290 Score: 2314.00 Matches: 421 Percent Similarity: 100.00\$ Conservative: 0 Conservative	21 LeuValSerTrpAspileProGlyAlaArgAlaLeuAspAsnGlyLeuAlaArgThrPro	DD 121 ACCATGGGGCTGCTGGGAGGCGCTTCATGTGGCAACCTTGACTGGCAGGAAGAGGCA 180 Qy 61 AspSerCysIleSerGluLysLeuPheMetGluMetAlaGluLeuMetValSerGluGly 80	Oy 81 TrpLysAspalaGlyTyrGluTyrLeuCysIleAspAspCysTrpMetAlaProGlnArg 100	Db 301 GATTCAGAAGGCAGACTTCAGGCAGCTTTCCTCATGGGATTCGCCAGCTA 360	Oy 141 ThrCysAlaGlyPheProGlySerPheGlyTyrTyrAspIleAspAlaGlnThrPheAla 160	Oy 161 AsptrpGlyValAspLeuLeuLysPheAspGlyCysTyrCysAspSerLeuGluAsnLeu 180 	Oy 181 AlaaspGlyTyrLysHisMetSerLeualaLeuasnargThrGlyArgSerllevalTyr 200	Oy 201 SerCysGluTrpProLeuTyrMetTrpProPheGlnLysProAsnTyrThrGluIleArg 220	Oy 221 GlnTyrCysAsnHisTrpArgAsnPheAlaAspIleAspAspSerTrpLysSerIleLys 240	Qy 241 SerileLeuAspTrpThrSerPheAsnGlnGluArgileValAspValAlaGlyProGly 260	Qy 261 GlyTrpAsnAspProAspMetLeuVall1eGlyAsnPheGlyLeuSerTrpAsnGlnGln 280 Db 781 GGTTGGAATGACCCAGATATGTTAGTGAATTGGCAACTTTGGCCTCAGCTGGAATCAGCAA 840	Qy 281 ValThrGlnMetAlaLeuTrpAlaIleMetAlaAlaProLeuPheMetSerAsnAsipLeu 300 Db 841 GTAACTCAGATGACCTCTGAGCTGCTCCTTTATTCATGTCTAATGACTC 900	Oy 301 ArgHis1leSerProGlnAlaLysAlaLeuLeuGlnAspLysAspValIleAla1leAsn 320	

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Patent No. 6887696

GENERAL INFORMATION:
APPLICANT: TURBEN, Thomas H.
APPLICANT: KUMAGAI, MONTO H.
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
FILE REFERENCE: 008010087CPUS06
CURRENT APPLICATION NUMBER: US/09/993,059
CURRENT APPLICATION NUMBER: US/09/993,059
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ORGANISM: Homo sapiens
FEATURE:
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US-09-993-059-9
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Best Local Similarity:
Query Match:
DB:
  ATG 1263
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	Oy 201 SerCysGluTrpProLeuTyrMetTrpProPheGlnLysProAsnTyrThrGluIleArg 220	Oy 221 GlutyrCysasnHisTrpargaenPheAlaaspIleaspaspSerTrpLysSerIleLys 240 	Qy 241 SerIleLeuAspTrpThrSerPheAsnGlnGluArgIleValAspValAlaGlyProGly 260	261 GlyTrpAsnAspProAspMetLeuVallleGlyAsnPheGlyLeuSerTrpAsnGlnGln 101	281 ValThrGlnMetAlaLeuTrpalaIleMetAlaAroLeuTheMetSerAsnAspLeu 281 ValThrGlnMetAlaLeuTrpalaIleMetAlaAlaAroLeuTheMetSerAsnAspLeu 841 GTAACTCAAATGGCCTACTGGGCTATCATGGCTGCTTTATTCATGTTAATGACTC	ArgHislleSerProGlnAlaLysAlaLeuLeuGlnAspLysAspVallleAlalleAsn 	321 GlnAspProLeuGlyLysGlnGlyTyrGlnLeuArgGlnGlyAspAsnPheGlu	341 GluargProLeuSerGlyLeuAlaTrpAlaValAlaMetIleAsnArgGlnGluileGly	1021 GAACGACCTCTCTCAGGCTTAGCCTGTAGCTATGATAAACCGGCAGGAGATTGGT 361 GlyProArgSerTyrThrIleAlaValAlaSerLeuGlyLygGlyValAlaCygABnPro	1081 GGACCICGCICIIAIACCAIGCAGIIGCIICCCIGGGIAAAGGAGIGGCCIGIAAICCI 381 AlaCygPheileThrGlnLeuleuProValLygArgLygLeuGlyPheTyrGluTrpThr	DD 1141 GCCTGCTTCATCACAGGTCCTCCCTGTGAAAAGGAAGGTAGGGTTCTATGAATGGACT 1200 Qy 401 SerArgLeuArgSerHisIleAsnProThrGlyThrValLeuLeuGlnLeuGluAsnThr 420 Db 1001 TCLLACCTTLLACTGCATTLLACTGCTATCACCTATCTCTTTCTTTCTTTCTTTTCT	421 Met 421	DD 1261 ATG 1263 RESULT 10 US-10-103-327-9	; Sequence 9, Application US/10103327 ; Datent No. 6890748 ; GENERAL INFORMATION: ; APPLICANT: GARGER, Stephen A.	; APPLICANT: TURPEN, Thomas H.; APPLICANT: KUMAGAI, Monto H.; APPLICANT: KUMAGAI, MONTO H.; TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN; TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION	; File Kerekence: Guodijos Chosolo; CURREN APPLICATION NUMBER: US/10/103,327; CURRENT FILING DATE: 2002-03-20; PRIOR APPLICATION NUMBER: US/09/993,059	; PRIOR FILING DATE: 2001-11-13; NUMBER OF SEQ ID NOS: 37; SOFTWARE: Fast SEQ for Windows Version 4.0; SEQ ID NO 9	; LENGTH: 1296 ; TYPE: DNA ; ORGANISM: Homo sapiens ; FEATURE:

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                             AspTrpGlyValAspLeuLysPheAspGlyCysTyrCysAspSerLeuGluAsnLeu
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US-09-993-059-5

Sequence 5, Application US/09993059

Fatent No. 6887696

GENERAL INFORMATION:
APPLICANT: GARGER, Stephen A.
APPLICANT: TURPEN, Thomas H.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION TITLE REFERENCE: 0080100097CPUSG6; CURRENT APPLICATION NUMBER: US/09/993,059

CURRENT FILING DATE: 2001-11-13

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSEQ for Windows Version 4.0

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                                                                                                                     SerileLeuAspTrpThrSerPheAsnGlnGluArgIleValAspValAlaGlyProGly
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AspTrpGlyValAspLeuLeuLysPheAspGlyCysTyrCysAspSerLeuGluAsnLeu
                         481 GACTGGGGAGTAGATCTGCTAAAATTTGATGGTTGTTACTGTGACAGTTTGGAAAATTTG
                                                     AlaAspGlyTyrLysHisMetSerLeuAlaLeuAspArgThrGlyArgSerlleValTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Sequence 18, Application US/08928881
| Patent No. 6083725
| GENERAL INFORMATION: THERAPY FOR ALPHA-GALACTOSIDASE A
| TITLE OF INVENTION: THERAPY FOR ALPHA-GALACTOSIDASE A
| TITLE OF INVENTION: DEFICIENCY
| TITLE OF INVENTION: STREET
| STREET: ADDIESSEE: FISH & Richardson
| STREET: MA
| COUNTY: USA
| COUNTY: USA
| COUNTY: USA
| CONPUTER READABLE FORM:
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US-08-928-881-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AspSerCysIleSerGluLysLeuPheMetGluMetAlaGluLeuMetValSerGluGly
                                                                                       Sequence 5, Application US/10103327
; Patent No. 6890748
; GENERAL INFORMATION:
APPLICANT: GARGER, Stephen A.
APPLICANT: TUREEN, Thomas H.
APPLICANT: KUMAGAI, Monto H.
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
FILE REFERENCE: 008010087CPUSO6
CURRENT APPLICATION NUMBER: US/10/103,327
CURRENT APPLICATION NUMBER: US/09/993,059
PRIOR PLING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
SOFTHARE: PastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH. 1308
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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; ORGANISM: Homo sapiens
; PEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1308)
US-10-103-327-5
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Pred. No.:
Score:
Percent Similarity:
1
Best Local Similarity:
1
Query Match:
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DB:
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1261 ATG 1263
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                                                                                               GlnTyrCysAsnHisTrpArgAsnPheAlaAspIleAspAspSerTrpLysSerIleLys
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ADDRESSEE: Fish & Richardson
STRRET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTY: USA
ZIATE: MA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Batantin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,921
FILING DATE: 06-Apr--2000
CLASSIFICATION: <Unknown>
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US-09-543-921-18
; Sequence 18, Application US/09543921
; Patent No. 6395884
; GENERAL INFORMATION:
; APPLICANT: Selden et al., Richard F.
; TITLE OF INVENTION: THERAPY FOR ALPHA-GALACTOSIDASE;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,881
FILING DATE:
CLASSITCATION: 435
ATTORNEY/AGENT INPORMATION:
NAMM: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/003001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
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Matches:
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Best Local Similarity:
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                 ValThrGlnMetAlaLeuTrpAlaIleMetAlaAlaProLeuPheMetSerAsnAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                381 AlacysPheIleThrGlnLeuLeuProValLysArgLysLeuGlyPheTyrGluTrpThr
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GlnTyrCysAsnHisTrpArgAsnPheAlaAsplleAspAspSerTrpLysSerIleLys
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APPLICANT: Selden, Richard F
APPLICANT: Selden, Marianne
APPLICANT: Borowski, Marianne
APPLICANT: Treco, Douglas A
APPLICANT: Treco, Douglas A
APPLICANT: Williams, Melanie D
APPLICANT: Schuetz, Thomas J
APPLICANT: Schuetz, Thomas J
APPLICANT: Daniel, Peter F.
TITLE OF INVENTION: Treatment for alpha-Galactosidase A Deficiency
FILE REFERENCE: FABRY DISEASE (18082-001)
CURRENT FAPLICATION NUMBER: US/09/266,014
CURRENT FILING DATE: 1996-09-13
PRIOR APPLICATION NUMBER: 06/026,041
PRIOR APPLICATION NUMBER: 06/28,881
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 24
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; TYPE: DNA
; ORGANISM: Homo sapiens
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421
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                                                           NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1343 base pairs
TPE: NOTOLES: single
STRANDEDNESS: single
TOPOLOGY: linear
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION DATA:

APPLICATION NUBBER: 08/928,881
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Db 936 CGACACATCAGCCCTCAAGCTCTTCAGGATAAGGACGTAATTGCCATCAAT 995 321 GlnAspProLeuGlyLysGlnGlyTyrGlnLeuArgGlnGlyAspAsnPheGluvalTrp 340 111	Search completed: December 26, 2005, 13:52:44 Job time : 250 secs
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PubMed=15772651, DOI=10.1038/nature03440;

Ross M.T., Graffnam D.V., Coffey A.J., Scherer S., McLay K., Muzny D.,

Platzer M., Howell G.R., Burrows C., Bird C.P., Frankish A.,

Lovell F.L., Howe K.L., Ashurst J.L., Fulton R.S., Sudbrak R., Wen G.,

Jones M.C., Hurles M.E., Andrews T.D., Scott C.E., Searle S.,

Ramser J., Whittaker A., Deadman R., Carter N.P., Hunt S.E., Chen R.,

Cree A., Gunaratne P., Havlak P., Hodgson A., Metzker M.L.,

Richards S., Scott G., Steffen D., Sodergren E., Wheeler D.A.,

Richards S., Annscough R., Ambrose K.D., Ansari-Lari M.A., Aradya S.,

Ashwell R.I., Babbage A.K., Bagguley C.L., Ballabio A., Banerjee R.,

Barker G.E., Barlow K.F., Barrett I.P., Bates K.N., Beare D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Signal sequence and DNA-mediated expression of human lysosomal alphagalactosidase A.";
Eur. J. Biochem. 165:275-280(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sixty-nine kilobases of contiguous human genomic sequence containing
the alpha-galactosidase A and Bruton's tyrosine kinase loci.";
Mamm. Genome 6:334-338(1995).
                                                                                                                                                                                                                                                                                                                          01-JAN-1988 (Rel. 06, Created)
01-ANG-1988 (Rel. 08, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Alpha-galactosidase A precursor (EC 3.2.1.22) (Melibiase) (Alpha-D-galactoside galactohydrolase) (Alpha-D-galactoside galactohydrolase) (Alpha-D-galactoside galactohydrolase)
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MEDLINE=59352959; PubMed=7626884;
Oeltjen J.C., Liu X., Lu J., Allen R.C., Muzny D.M., Belmont J.W.,
Gibbs R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-89263745; PubMed-2542896;
Kornreich R., Desnick R.J., Bishlop D.F.;
"Nucleotide sequence of the human alpha-galactosidase A gene.";
Nucleic Acids Res. 17:3301-3302(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
TISSUB-Fibroblast;
MEDLINE=81246603; PubMed=3036505;
Tsuji S., Martin B.M., Kaslow D.C., Migeon B.R., Choudary P.V., Stubblefield B.K., Mayor J.A., Murray G.J., Barranger J.A., Ginns B.I.;
                          05xtz3
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 Homo sapiens (Human).
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TISSUE=Lymphoblast;
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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2: uniprot_trembl:*
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Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki
Tanaka A., Yokoyama S.;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AK222627; BAD96347.1; -; mRNA.
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Maruyama K., Sugano S.;
"Oligo-capping: a simple method to replace the eucaryotic mRNAB with oligoribonucleotides.";
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Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
Phelan M., Farmer A.;
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                                                                                         Length 429;
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                                                                                                                                      Indels
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Last annotation update)
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                                                                                    Query Match 100.0%; Score 2314; DB 1; Best Local Similarity 100.0%; Prad. No. 2.8e-187; Matches 421; Conservative 0; Mismatches 0;
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J. Clin. Invest. 83:1390-1399(1989)
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NUCLEOTIDE SEQUENCE.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
Homo.
                                                                                                                         SILDMTSFNQERIVDVAGPGGWNDPDMLVIGNFGLSWNQQVTQWALMAIMAAPLFMSNDL
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Bishop D.F., Calhoun D.H., Bernstein H.S., Hantzopoulos P., Quinn M.,
Desnick R.J.;
                                                                                                                                                                                        ADGYKHMSLALNRTGRSIVYSCEWPLYMWPFQKPNYTBIRQYCNHWRNFADIDDSWKSIK
                                                                                                                                                                                                                                                                                   SILDWISFNQERIVDVAGPGGWNDPDMLVIGNFGLSWNQQVTQMALWAIMAAPLFMSNDL
                                                                                              ANYVHSKGLKLGIYADVGNKTCAGFPGSFGYYDIDAQTFADWGVDLLKFDGCYCDSLENL
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GO; GO:0004557; F:alpha-galactosidase activity; IEA.

GO; GO:0004557; F:alpha-galactosidase activity; IEA.

GO; GO:0004553; P:hydrolase activity, hydrolyzing O-glycosyl . . .

GO; GO:0005957; P:carbohydrate metabolism; IEA.

InterPro; IPR002241; Glyco_hydro_GHD.

Frant. PF02065; Mellibase; 1.

PRINTS; PR00740; GLHYDRLASE27.

PRODOM; PB002522; Glyco_hydro_GHD; 1.

PROSITE; PS00512; ALPHA_GALACTOSIDASE; 1.

Glycosidase; Hydrolase.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Alpha-galactosidase A (EC 3.2.1.22) (Fragment).
Name=alpha-GalA;
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TISSUE=Lung;
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Gaps

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Matches 395; Conservative

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                                                                      YMWPFOKPNYTEIROYCHHWRNFADIDDSWKSIKSILDWTSFNOERIVDVAGPGGWNDPD
                                                                                                                                                                                                                                                     MLVIGNPGLSWNQQVTQWALWAIMAAPLFWSNDLRHISPQAKALLQDKDVIAINQDPLGK
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Mus musculus (Mouse).
Bukarvota; Matazao; Crordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchoncoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Mus
EYLCIDDCWMAPQRDSEGRLQADPQRFPHGIRQLANYVHSKGLKLGIYADVGNKTCAGFP
                                                                                                                   GSFGYYDIDAQTFADWGVDLLKFDGCYCDSLENLADGYKHMSLALNRTGRSIVYSCEWPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6; TISSUB=Kidney; MEDLINE=96125203; PubMed=8543175; DOI=10.1016/0378-1119(95)00592-7; Obshima T., Murray G.J., Nagle J.M., Quirk J.M., Kraus M.H., Barton N.W., Brady R.O., Kulkarni A.B.; Tructural organization and expression of the mouse gene encoding alpha-galactosidase A.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-077-1996 (Rel. 34, Created)
01-077-1996 (Rel. 34, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Alpha-galactosidase A precursor (EC 3.2.1.22) (Melibiase) (Alpha-D-galactoside galactohydrolase) (Alpha-D-galactoside galactohydrolase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-95352959; PubMed=7626884;
Oeltjen J.C., Liu X., Lu J., Allen R.C., Muzny D.M., Belmont J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDILINE-56316016; PubMed-8733892; DOI=10.1006/bmme.1996.0020; Gotlib R.W., Bishop D.F., Wang A.M., Zeidner K.M., Ioannou Y.I., Adler D.A., Disteche C.M., Desnick R.J.; "The entire genomic sequence and cDNA expression of mouse alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sixty-nine kilobases of contiguous human genomic sequence con
the alpha-galactosidase A and Bruton's tyrosine kinase loci.";
Mamm. Genome 6:334-338(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=FVB/N; TISSUE=Mammary gland;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                     LLPVKRKIGFYEWTSRLRSHINPTGTVLLQLENTM 421
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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alaener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheez T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S.W., Worley V.M., Sodergren E.J., Lu X., Gibbs R.A.,
Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Willalon D.K., Muzny D.M., Scherger B.J., Lu X., Gibbs R.A.,
Allakealey R.W., Touchman A., Young A.C., Shevchenko Y., Boutfard G.G.,
Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Feneration and initial analysis of more than 15,000 full-length human
mouse cDNA sequences.";
For CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing alpha-D-
Gligosaccharides, galactomannans and galactosee.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alphamilarity of the property of the process of the property o
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-i- SIMILARITY: Belongs to the glycosyl hydrolase 27 family.
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ProDom; PD002572; Glyco_hydro GHD; 1.
PROSITE; PS00512; ALPHA_GALACTOSIDASE; 1.
Glycoprotein; Glycosidase; Hydrolase; Lysosome; Signal.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U34071; AAA96749.1; -; mRNA.
EMBL; L46651; AAA74453.1; -; Genomic_DNA.
EMBL; U58105; AAB47244.1; -; Genomic_DNA.
EMBL; U50716; AAC52584.1; -; mRNA.
EMBL; U50715; AAC52583.1; -; Genomic_DNA.
EMBL; BC009021; AAH09021.1; -; mRNA.
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SMR; P51569; 32-418.
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KEALIMECIAD. SEQUENCE.

STRAIM-CSTENL/GI. TISSUE-OVARTY, and Thymus;

KAWAI J., Shinagawa A., Shibata K., Yoshino M., Ichoh M., Ichil Y.,

RAWAI J., Shinagawa A., Shibata K., Yoshino M., Ichoh M., Ichil Y.,

A Arawawa T., Hara A., Fukunishi X., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Azawa K., Izawa M., Nishi K., Shoon H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavannt T.,

Radota K., Matsuda H.A., Shibata K., Caniwa H.,

Radota K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Hayashizaki Y.,

Hayashizaki Y.,
                ANYVHSKGLKLGIYADVGNKTCAGFPGSFGSYDIDAQTFADWGVDLLKFDGCHCDSVVSL 180
                                                                                                                                                        181 ADGYKHMSLALNRTGRSIVYSCEWPLYMWPFQKPNYTEIRQYCNHWRNFADIDDSWKSIK 240
                                                                                                                                                                               ANYVHSKGLKLGIYADVGNKTCAGFPGSFGYYDIDAQTFADWGVDLLKFDGCYCDSLENL 180
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DSCISEKLFMEWAELMVSEGWKDAGYEYLCIDDCWMAPQRDSEGRLQADPQRFPHGIRQL
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-FBB-2005 (TrEMBLrel. 29, Last amotation update)
Mus musculus 0 day neonate thymus CDNA, RIKEN full-length enriched
library, clone:A430057F16 product:galactosidase, alpha, full insert
sequence (Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN
full-length enriched library, clone:E330039P08 product:galactosidase,
alpha, full insert sequence).
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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Bukaryotei, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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QBBGZ6;
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Matches 327; Conservative

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Local Similarity

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RA MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Mikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Majarelli R., Haill D.P., Bult C., Hune D.A., Quackenbush J.,

RA Baldarelli R., Hill D.P., Bult C., Hune D.A., Quackenbush J.,

RA Baldarelli R., Hill D.P., Bult C., Hune D.A., Quackenbush J.,

RA Baldarelli R., Hill D.P., Bult C., Hune D.A., Quackenbush J.,

RA Gasterland T., Gariboldi M., Gissi C., Corbani L.E., Cousins S.,

RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Gasterland T., Maxedyi H., Kawasawa N., Jackson I.J., Jarvis B.D.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.L.,

RA Ravasi T., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Wilming L.G., Wyrshaw Boris A., Yang I., Yang I.,

RA Wilming L.G., Wyrshaw Boris A., Yang I., Yang I.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Hara A., Hashizume W., Imocani W., Ishing Y., Itoh M., Kagawa I.,

RA Mayazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Hara A., Hashizume W., Materston R., Lander E.S., Rogers J.,

RA Manalysis of the mouse transcriptome based on functional annotation of

RA Warna A., Legal C. PONAS.

RA Malysis of the mouse transcriptome based on functional annotation of
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STRAIN=C57BL/6J; TISSUB=Ovary, and Thymus;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Hukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayashida K., Hariamoto K., Hirzoka T., Hirzokane T., Ayashida Y., Inchani K., Ishili Y., Itoh M., Kadawa T., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Nishi K., Nomura K., Ninazaki R., Sakazume N., Sano H., Sato R., Saito R., Sakio K., Sakazume N., Sano H., Takaku-Akahira S., Takeda Y., Tagami M., Tomaru A., Takahahi P., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Lonaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
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STRAIN=CSTBL/65; TISSUE=Ovary, and Thymus;
STRAIN=2013; Pubmed=11076861; DOI=10.1101/gr.152600;
A MEDLINE=2030913; Pubmed=11076861; DOI=10.1101/gr.152600;
A Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishiia Y., Makamura S., Hazama M., Nishine T., Harada A., A vamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., A vamamoto R., Inoue K., Togawa Y., Izawa M., Ohara E., Matshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., A Okazaki Y., Muramateu M., Inoue Y., Kira A., Hayabhizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
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   'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                               STRAIN=C57BL/6J; TISSUE=Ovary, and Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 420:563-573 (2002).
                                          Nature 409:685-690(2001)
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 SILDWISFNGERIVDVAGPGGWNDPDMLVIGNFGLSWNQQVTQMALWAIMAAPLFMSNDL 300
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
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                                                                                                                                                                                                                                                                                                             Length 421;
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AA290422; CAC44626.1; -; Genomic_DNA.
HSSP; P06289; 1R46.
Ensembl; SINFRUG0000147523; Fugu rubripes.
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                                                                                                                                                                                                                                                               421 AA; 47844 MW; SF66772334014B6F CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                          78.2%; Score 1811; DB 2; 78.2%; Pred. No. 1.1e-144; ive 41; Mismatches 50;
EMBL, AK040081; BAC3508.1; -; mRNA.

EMBL, AK054547; BAC35819.1; -; mRNA.

HSSP, P06280; 1R46.

SMR; QBBGZ6; 34-420.

MGI; MGI:1347344; Gla.

GO; GO:0005615; C:extracellular space; TAS.

InterPro; IPR00111; Glyco_hydro_27.

InterPro; IPR00111; Glyco_hydro_GHD.

Pfam; PF02065; Melibiase; I.

PRINTS; PR00740; GLHYRLASE27.

PROSTTE; PS00512; ALPHA GALACTOSIDASE; 1.

PROSTTE; PS00512; ALPHA GALACTOSIDASE; 1.

SEQUENCE 421 AA; 47844 MW; 5F66772334014BE
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-UNN-2003 (TrEMBLrel. 24, Last ann
Alpha galactosidase a.
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Matches 327; Conservative
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Submitted (JUL-2001)
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                                                                                                                                                                                                                                                                                                                 Query Match
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the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
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Matches 227; Conservative
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QSXJT6;
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                                                                                                                                                                                                preliminary data.
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WICLEOTIDE SEQUENCE.

WICLEOTIDE SEQUENCE.

WICLEOTIDE SEQUENCE.

WAS AllON O., AUYY J.M., Brunet F., Petit J.L., Stange-Thomann N.,
Manceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Macaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Biemont C., Salanoubat M., Levy M., Boulain J., De Berardinis V.,
Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
Rellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                           7
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                                                                                                                                                                                                                                                                                                                                                                                 7 ALVFLIGPAAEALDNGLALTPTMGWLHWERFMCNTDCDQDPDNCISERLFMQVADVMVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KTCAGFPGSFGYYDIDAQTFADWGVDLLKFDGCYCDSLENLADGYKHMSLALNRTGRSIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 YSCEWPLYEWRFQKPNYTAIRETCNHWRNSADVLDSWSSIKSISAWTADYQDTIVPAAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGWNDPDMLVIGNFGLSWNQQVTQMALWAIMAAPLFMSNDLRHISPQAKALLQDKDVIAI
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostel, Euteleostel, Neoteleostei, Acanthomorpha, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes; Tetradontoidea, Tetraodontidae, Tetraodon.
GO; GO:0004553; P:hydrolase activity, hydrolyzing O-glycosyl . . . GO; GO:0005975; P:carbohydrate metabolism; IEA. InterPro; IPR005241; Glyco_hydro_27. InterPro; IPR00111; Glyco_hydro_GHD. Pf02065; Melibiase; I.
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                                                                                                                                                                                                                                            2; Length 429;
                                                                                                                                                                                                                                                                                        72; Indels
                                                                                                                                                                                        48480 MW; 536A826D520CF01C CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 1 SCAF14998, whole genome shotgun sequence.
ORFNames=GSTENG00029285001;
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PACNVTQILPHYKDMGVQPMFSKMVVRVNPSGTVLL 399
                                                                                                                                                                                                                                     Query Match
64.0%; Score 1480.5; DB 2;
Best Local Similarity 68.4%; Pred. No. 1.1e-116;
Matches 271; Conservative 50; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 377 AA
                                                                                                                   PRINTS; PR00740; GLHYDRLÄSE27.
Probom; PD002572; Glyco hydro GHD; 1.
PROSITE; PS00512; ALPHA GALACTOSIDASE;
SEQUENCE 429 AA; 48480 NW; 536A826f
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Q4RTE7;
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derged J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Woore T., Max S.I., Wang J., Hong L.,

Brownstein M.J., Woldin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabs R.A.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                       LMVSEGWKDAGYEYLCIDDCWMAPQRDSEGRLQADPQRFPHGIRQLANYVHSKGLKLGIY
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                                                                                                                                                                                                                                                                                                                                                                                        16 LRFLALVSWDI-PGARALDNGLARTPTMGWLHWERFMCNLDCQEEPDSCISEKLFMEMAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                            CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                            2;
                                                                                                                                                                                                                                                            Length 377;
      Genome Research;
                                                                                                                                                                                                                                                                                                                        48; Indels
Genoscope, Whitehead Institute Centre for Genome Research
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                    CAAE01014998; CAG08335.1; -; Genomic DNA.
NCE 377 AA; 42048 MW; 236F4E5A95B9F1A8 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                        54.8%; Score 1267; DB 2; 72.1%; Pred. No. 1.2e-98; ive 38; Mismatches 48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46 GLKLGIYADVGTKTCAGYPGSLGYYDIDAKTFADWGVDLLKFDGCFMPDWHQLGEGYINM 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLALNRIGRSIVYSCEWPLYMWPPOKPNYTEIRQYCNHWRNFADIDDSWKSIKSILDWTS 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FNGERIVDVAGPGGWNDPDMLVIGNFGLSWNQQVTQMALWAIMAAPLFMSNDLRHISPQA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLKLGIYADVGNKTCAGFPGSFGYYDIDAQTFADWGVDLLKFDGCYCDSLENLADGYKHM 187
                                                                                                                                                                  NUCLEALLY

TISSUE-Embryo;

Director MGC Project;

Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.

Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; BC0813209; AAH83209.1; -; mRNA.

ZFIN; ZDB-GENE-041010-207; zgc:101584.

GO; GO:0004553; F: hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.

GO; GO:0005975; P: carbohydrate metabolism; IEA.

InterPro; IPR00111; Glyco_hydro_GHD.

InterPro; IPR00111; Glyco_hydro_GHD.

PR.NTS; PR00740; GLHYDRLASE27.

PRODOM; PD002572; Glyco_hydro_GHD: 1.

SEQUENCE 338 AA; 37846 WW; A3FC5C461B7C9649 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LDMSLCALMIA-GLRNKG-----THRGACRQTPKGFPVASKKLADYVHSK 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KALLODXDVIAINODPLGKOGYOLRQGDNFBVWERPLSGLAWAVAMINRQEIGGPRSYII
                                                              human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Bulterfield Y.S.N., Krzywinski M.L., Skalska U., Smailus D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.; Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length and initial analysis of more than 15,000 full-length and initial analysis of more than 15,000 full-length and and initial analysis of more than 15,000 full-length and and analysis of more than 15,000 full-length and 15,0
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.8%; Score 1130; DB 2; 60.3%; Pred. No. 4.1e-87; iive 47; Mismatches 75;
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Name=LOC443592;
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QGQ17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210; Conservative
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8355;
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Q6GQ17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .; IEA.
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Braha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEman P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Paney J., Helton E., Ketteman M., Madan A., Kodrigues S., Sanchez A., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Butterfield Y.S.M., Krzywinski M.I., Skalska W.M., Schnetch A., Schein J.E., Jones S.J.M., Marra M.A.; Schnetch A., Schein J.E., Jones S.J.M., Marra M.A.; Smailus D.E., Schnetch A., Schein J.E., Jones S.J.M., Marra M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 VHSKGLKLGIYADVGNKTCAGFPG-SFGYYDIDAQTFADWGVDLLKFDGCYCDSLENLAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klein S., Gerhard D.S.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC072931; AH72931.1; -; mRNA.
GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl ...
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR002241; Glyco.hydro_G7.
InterPro; IPR000111; Glyco.hydro_GHD.
PF02065; Meliblase; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genetic and genomic tools for Xenopus research: The NIH Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.4%; Score 1074.5; DB 2; Length
49.3%; Pred. No. 2.8e-82;
tive 62; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4C578DB433983471 CRC64;
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ProDom; PD002572; Glyco_hydro_GHD; 1.
PROSITE; PS00512; ALPHA_GALACTOSIDASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431 AA; 48787 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    initiative.";
Dev. Dyn. 225:384-391(2002)
                                                                                                                                                                                                                                                                                                                                                           mouse cDNA sequences."
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Matches 209; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
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SEQUENCE
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WEDINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hasteh F.,
Diatchenko L., Marusina K., Farner A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzuy D.M., Sodergran R.J., Lu X., Gibbs R.A.,
A Willalon D.K., Muzuy D.M., Sodergran B.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakealey R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Green B.D., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Generation and initial analysis of more than 15,000 full-length human
The Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Ovary;

Klein S., Gerhard D.S.;

Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.

Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; BCO71089; AAH71089.1; -; mRNA.

GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . .; IEA.

GO; GO:0005975; P:carbohydrate metabolism; IEA.

InterPro; IPR000241; Glyco_hydro_GHD.

PRAMTY; PR00065, Mellbiase; I.

PROMO76, GLHYDRASE27.

PROMO76, GHYDRASE27.

PROMO76, CHAPRASE27.

PROMO76, SHYDRASE27.

PROMO76, AMB GALACTOSIDASE; I.

PROSITE; PS00512; ALPHA_GALACTOSIDASE; I.
                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoldea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.7%; Score 1056.5; DB 2; Length 400; 51.0%; Pred. No. 8.5e-81; ive 58; Mismatches 114; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                               400 AA.
                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                       Xenopodinae; Xenopus; Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 51.0%;
Matches 201; Conservative
                                                                                                                             OGGR44 XENLA PRELIMINARY;
Q6GR44;
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                                                                                                                                                                                                                         MGC81044 protein.
Name=MGC81044;
LLOL 417
                                   421 FLFL 424
                                                                                                                                                                                                                                                                                                                                         NCBI TaxID=8355;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                      306 LISQVGSLEVWKRELINGQYAVAVLNKGTDGLPRPYTTSLGLLN-----ITQCTD 355
                                                                 DDCWMAPQRDSEGRLQADPQRFPHGIRQLANYVHSKGLKLGIYADVGNKTCAGFPG-SFG 150
                                                                                                                                                    151 YYDIDAQTFADWGVDLLKFDGCYCDSLENLADGYKHMSLALNRTGRSIVYSCEWPLYMWP 210
                      99
186 LPPKVNYTQLGSICNMWRNYGDIQDSWDSVLDIIEWYAKNQDVLQPAAGPGRWNDPDMLI
                                                                                                                                                                                                                                                                                                                            270 IGNFGLSWNQQVTQMALWAIMAAPLFMSNDLRHISPQAKALLQDKDVIAINQDPLGKQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-SEP-2005 (Rel. 48, Created)
13-SEP-2005 (Rel. 48, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Alpha-N-acetylgalactosaminidase (EC 3.2.1.49) (Alpha-galactosidase B).
                                                                                                                                                                                                                                         211 F-QKPNYTEIRQYCNHWRNFADIDDSWKSIKSILDWTSFNQERIVDVAGPGGWNDPDMLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Structure 10:425-434(2002).
--- CATALYITC ACTIVITY: Hydrolysis of terminal non-reducing N-acetyl-b-galactosamine residues in N-acetyl-alpha-D-galactosaminides.
--- SUBCELLULAR LOCATION: Lysosomal (By similarity).
--- SIMILARITX: Belongs to the glycosyl hydrolase 27 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94060104; PubMed=8241271; DOI=10.1016/0167-4781(93)90158-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

PubMed=12005440; DOI=10.1016/S0969-2126(02)00726-8;

Garman S.C., Hannick L., Zhu A., Garboczi D.N.;

The 1.9 A structure of alpha-N-acetylgalactosaminidase: molecular basis of 91ycosidase deficiency diseases.";

Structure 10:425-434(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Davis M.O., Hata J., Smith D., Walker J.C.; "Cloning and sequence of a chicken alpha-N-acetylgalactosamindase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [MRNA], AND PARTIAL PROTEIN SEQUENCE. IISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              356 GYKMYNVFEKEYIGMFKSGIPIDMRVNPIGVIFL 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----VKRKLGFYEWTSRLRSHINPTGTVLL 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         405 AA
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PDB; IKTB; X-ray; A=1-405.
PDB; IKTC; X-ray; A=1-405.
Ensembl; ENSGALG0000011900; Gallus gallus.
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5

21; Gaps

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410
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ORFNames=GSTENG00012743001;
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Q4STX0;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 193; Conservative
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                    SEQUENCE
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 F-QKPNYTEIRQYCNHWRNFADIDDSWKSIKSILDWTSFNQERIVDVAGPGGWNDPDMLV 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGNFGLSWNQQVTQMALWAIMAAPLFMSNDLRHISPQAKALLQDKDVIAINQDPLGKQGY 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q-LRQGDNFEVWERPLSGLAWAVAMINRQEIGGPRSYTIAVASIGKGVACNPACFITQLL 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDCWMAPQRDSEGRLQADPQRFPHGIRQLANYVHSKGLKLGIYADVGNKTCAGFPG-SFG 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDNGLARTPTMGWLHWERFMCNLDCQEEPDSCISEKLFMEMAELMVSEGWKDAGYEYLCI
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
InterPro; IPR002241; Glyco_hydro_27.
InterPro; IPR000111; Glyco_hydro_GHD.
Pfam; PP02065; Melibiase; 1.
Promy Pr0740; GHYDRLASE27.
Probom; P0002572; Glyco_hydro GHD; 1.
PROSITE; PS00512; ALPHA_GALACTOSIDASE; 1.
3D-structure; Direct protein sequencing; Glycoprotein; Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
                                                                                                                                                         Alpha-N-acetylgalactosaminidase.
Nucleophile (By similarity).
Proton donor (By similarity).
N-linked (GlCNAC...).
N-linked (GlCNAC...).
N-linked (GlCNAC...).
                                                                                                                                                                                                                                                                                                                                                                                                 45.4%; Score 1051; DB 1; Length 405; llarity 53.0%; Pred. No. 2.5e-80; Conservative 58; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Anopheles gambiae Sequence Committee; "Anopheles gambiae re-annotation."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                            45615 MW; E1EC0061739C305C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
101-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANGED0000020647 (Fragment).
ORFNames=ENSANGG0000018358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVKRKLGFYEWISRLRSHINPIGTVLLQL 417
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Q7Q1V0;
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NUCLEOTIDE SEQUENCE.
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405 AA;
                                                                                                                                             Hydrolase; Lysosome
                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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CARBOHYD
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CARBOHYD
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91 IDDCWMAPQRDSEGRLQADPQRFPHGIRQLANYVHSKGLKLGIYADVGNKTCAGFPGSFG 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 AGMNPNYSSIIQHCNLWRNYDDIQDSWASLESIIDYYGNNQDAIIPNAGPGHWNDPDMLI 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 ALDNGLARTPTMGWLHWERFWCNLDCQEEPDSCISEKLFMEMAELMVSEGWKDAGYEYLC 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLENGLARTPPMGMLSWERFRCNTDCEGDPENCISEHLFRTWADLVVSEGYAAVGYEYIN 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Eukaryota; Metazoa; Chordata; Cramiata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Cramiata; Vertebrata; Neoteleostei;
Actinopterygii; Neopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAP14084, whole genome shotgun sequence.
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                                                                                                                                    preliminary data.

EMBL, AAABOL008980; EAA14548.2; -; Genomic DNA.

GO; GO:0004553; P:hydrolase activity, hydrolyzing O-glycosyl.

GO; GO:0005975; P:carbohydrate metabolism; IEA.

InterPro; IPR002241; Glyco_hydro_27.

InterPro; IPR00111; Glyco_hydro_GHD.

Pfam; PF02065; Melibiase; I.

PRINTS; PR00740; GLHYDRLASE27.

ProDom; PD002572; Glyco_hydro_GHD; 1.
                                                                                                   which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.4%; Score 1050; DB 2; Length 4
49.0%; Pred. No. 3.1e-80;
ive 72; Mismatches 119; Indels
The Anopheles gambiae Sequence Committee;
Submitted (APR-2004) to the EMBL/GenBamk/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46517 MW; 4C91C8FB9EA6C88F CRC64;
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Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
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Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Blemout C., Skalli Z., Catcolico L., Poulain J., De Berardinis V., Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kellis M., Volff JN., Guigo R., Zody M.C., Meslrov P., Bosak S., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Blaudet V., Schachter V., Quetier F., Saurin W., Scarpelli C., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.; "Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype.";
                                                                                                                                                                                                                                                                                                                    LHLGCALALRFLALVSWDIPGARALDNGLARTPTMGWLHWERFMCNLDCQEEPDSCISEK
                                                                                                                                                                                                                                                                                                                                 GLKLGI YADVGNKTCAGFPGS-FGYYDIDAQTFADWGVDLLKFDGCYCDSLENLADGYKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 TSFNQERIVDVAGPGGWNDPDMLVIGNFGLSWNQQVTQMALWAIMAAPLFMSNDLRHISP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                306 QAKALLQDKDVIAINQDPLGKQGYQL-RQGDNFEVWERPLSGLAWAVAMINRQEIGGPRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        MSLALNRTGRSIVYSCEWPLYMWPF-QKPNYTEIRQYCNHWRNFADIDDSWKSIKSILDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365 YTIAVASLGKGVACNPACFITQLLPVKRKLGFYE----WTSRLRS-----HINPTG
                                                                                                                                                                                                                                                                                                42; Gaps
                                                                                                                                                                      Genoscope, Whitehead Institute Centre for Genome Kebearcu;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                        DB 2; Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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                                                                                                                                                                                                                                                  410 AA; 46172 MW; F5C661DA72DCEE88 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
CG5731-PA.
                                                                                                                                                                                                                                                                        Query Match

44.9%; Score 1038; DB 2;
Best Local Similarity 48.9%; Pred. No. 3.2e-79;
Matches 207; Conservative 58; Mismatches 116;
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3R 410 410
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                                                                                                                                                                                                                  preliminary data.
                                                                                                                                                          NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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RW UUCLEOTIDE SEQUENCE.

RA MEDIANE-2196006; PubMed=10731132; DDI=10.1126/science.287.5461.2185;

Adams M.D. Celliker S.E. I. Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celliker S.E. I. Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celliker S.E. I. Holt R.A., Evans C.A., Gocayne J.D.,

RA George R.A., Newis S.E., Richards S., Amburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Alampe M., Fleiffer B.D.,

RA Bardon R.C., Rogars Y.-H.C., Blazel R.G., Champe M., Fleiffer B.D.,

RA Bardon R.C., Rogars Y.-H.C., Blazel R.G., Champe M., Fleiffer B.D.,

RA Ballew R.M., Basu A., Barendal J., Bayrakteroglu L., Bessley E.M.,

Ballew R.M., Basu D.A., Berman B.P., Bhandari D., Bolshakov S.,

RA Ballew R.M., Cawley S., Dallke C., Davrengort L.B., Davies P.,

Buttis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Buttis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

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RA Ballew R.M., Delcher A., Deng Z., Mays A.D., Dew I., Diet Z. S.M.,

RA Pathos B., Delcher A., Bownes M., Dugan-Rochs S., Dunkov B.C., Dunn P.,

Durbin K.J., Evangelista C.C., Perrac C., Ferrica S., Fleischmann W.,

RA Harris N.L., Harvey D.A., Heiman T.J., Herandez J.R., Houck J.,

RA Harris N.L., Harvey D.A., Heiman T.J., Wei M.-H., Ibegwam C.,

Adalali M., Kalush F., Karpen G.H., Ka Z., Kannison J.A.,

RA Harris N.L., Marvey D.A., Heiman T.J., Wein M.P., Morberson D.,

RA Harris N., Wattei B., McInchoff T.C., Morris J., Moshrefi A.,

RA Liu X., Mattei B., McInchoff T.C., Morris J., Moshrefi A.,

Rount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nalson D.L.,

RA Balzacolo M., Pittman G.S., Pan S., Pollard J., Mang X.,

Ranger K., Spradling A.C., Staplecon M., Stupsk M. P., Smith T.,

Ranger K., Spradling A.C., Staplecon M., Stupsk M. Wang Z.-Y., Wassarman D.A., Weinsteen B., Sheel S., Pan R., Pollard Y., Shun E.,

Ranger R., Spradling A.C., Staplecon M., Stupsk M. Shun S.,

RA Rheng X.H., Zhong F.W., Zhong W., Zho
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MEDLINE-22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas Patel S., Prise B., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Intact, 09/127; ...
Ensembl; CG5731; Drosophila melanogaster.
FlyBase; FBGN03192; CG5731.
GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
GO; GO:0005575; P:carbohydrate metabolism; IEA.
InterPro; IPR00241; Glyco_hydro_27.
InterPro; IPR00241; Glyco_hydro_GHD.
Fam; PF02065; Melibiase; I.
FRUNTS; PR00740; GLHYDRIASE27.
FROSTITE; PS00512; ALPHA GALACTOSIDASE; 1.
SEQUENCE 413 AA; 47047 MW; 9ADE417E7592782D CRC64;
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                                                                                                                                                                                                         Berkeley Drosophila Genome Project; Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R. Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith Yu C., Rubin G., Rubin G., Branding melanogaster release 4 sequence."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Lewis S.E.; aAnnotation of the Drosophila melanogaster euchromatic genome: a systematic review."; Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 44.6%; Score 1031; DB 2; Length 413; Best Local Similarity 46.7%; Pred. No. 1.3e-78; Matches 192; Conservative 81; Mismatches 126; Indels 1.
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Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003627; AAF52871.2; -; Genomic_DNA.
HSSP; Q90744; 1KTB.
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Search completed: December 24, 2005, 08:58:15 Job time: 234 secs

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AR654962 Sequence
AR653697 Sequence
CS135670 Sequence
AR653692 Sequence
AR653692 Sequence
AR653693 Sequence
AY889631 Synthetic
AY889631 Synthetic
AY8892090 Synthetic
AY882039 Synthetic
AR853695 Sequence
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AR63691 Sequence
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Unknown.
Unclassified.
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I (bases 1 to 1266)
Garger, S.J., Turpen, T.H. and Kumagai, M.H.
Garger, S.J., Turposowal enzymes in plants by transient expression
Patent: US 6887696-A 11 03-MAY-2005,
Large Scale Biology Corporation; Vacaville, CA
Location/Qualifiers
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Sequence 11 from patent US 6887696.
AR653696
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  AR654962
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AR654965
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BT006864
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AR654963
BD185988
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    ORIGIN
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-MODEL=frame+ p2n.model -DEV=xlp
-MODEL=frame+ p2n.model -DEV=xlp
-Q=/Cgn2 1/USPTO gpool p/US10602219/runat_23122005_151141_17136/app_query.fasta_1.583
-Q=/Cgn2 1/USPTO gpool p/US10602219/runat_23122005_151141_17136/app_query.fasta_1.583
-DBCALGENDO - TRE_SERVET - END=-1 -MATRIX=D109um62 - TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 - END=-1 -MATRIX=D109um62 - TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 - END=-1 - MATRIX=D109um62 - ALIGN=15 - MODE_LOCAL
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-NO_WMAP - LARGEQUERY - NEG_SCORES=0 - WAIT - DSPBALCOK=100 - LONGLOG
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-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - PGLOP=6 - DELEXT=7
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E 1 (bases 1 to 1266)

S Gargers.J. Turpen, T.H. and Kumagai, M.H.
Production of lysosomal enzymes in plants by tra
Production of lysosomal enzymes in plants by tra
Patent: US 6890748-A 11 10-MAY-2005;
Large Scale Biology Corporation; Vacaville, CA
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Db 1141 GCCTGCTTCATCACACACACCTCCTGTGAAAAGGAAGCTAGGGTTCTATGAATGGACT 1200	Qy 401 SerArgLeuArgSerHisIleAsnProThrGlyThrValLeuLeuGluLeuGluAsnThr 420 Db 1201 TCAAGGTTAAGAAGTCACATAAATCCCACAGGCACTGTTTTGCTTCAGCTAGAAAACACA 1260	Ογ 421 Met 421	1261	5 7 AR653697 ION Sequence 13 ON AR653697	VEXWORDS UNKNOWN.	Unclassified. REFERENCE T. 1284) AUTHORS Garger, S.J., Turpen, T.H. and Kumagai, M.H. TITLE Production of lysosomal enzymes in plants by transient expression	OUNKNAL FACENC: US 588/559-74 13 U3-MAI-20U3; EATURES Location/Qualifiers BOUICE 1. 1284	/organism="unknown" /mol_type="genomic DNA" ORIGIN	Alignment Scores: 1.36e-207 Length: 1284 Score: 2314.00 Matches: 421 Percent Similarity: 100.00* Conservative: 0	Mismatches: Indels: Gaps:	US-10-602-219-12 (1-421) x AR653697 (1-1284) Qy	Db 1 ATGCAGCTGAGGAACCCAGAACTACATCTGGGCTGGGGCTTGGGTTCGGTTCCTGGCC 60 Qy 21 LeuValSerTrpAspIleProGlyAlaArgAlaLeuAspAsnGlyLeuAlaArgThrPro 40 L	41 ThrmetGlyTrpLeuHisTrpGluArgPheMetCysAsnLeuAspCysGlnGluGluPro	Qy 61 AspSerCysIleSerGluLysLeuPheMetGluMetAlaGluLeuMetValSerGluGly 80 	Oy 81 TrpLysAspalaGlyTyrGluTyrLeuCysIleAspAspCysTrpMetAlaProGlnArg 100 	Oy 101 AspSerGluGlyArgLeuGlnAlaAspProGlnArgPheProHisGlyIleArgGlnLeu 120 	Oy 121 AlaAsnTyrValHisSerLy8GlyLeuLysLeuGly11eTyrAlaAspValGlyAsnLys 140 	Oy 141 ThrCysAlaGlyPheProGlySerPheGlyTyrTyrAsp1leAspAlaGlnThrPheAla 160 141 ThrCysAlaGlyPheProGlySerPheGlyTyrTyrAsp1leAspAlaGlnThrPheAla 160 141

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Crystal structure of human a-galactosidase
Patent: WO 2005069192-A 1 28-JUL-2005;
Transkaryotic Therapies, Inc. (US); Selden, Richard F. (US);
Tagarboczi, David N. (US); Treco, Douglas A. (US); NIH/NIAID (US);
Garman, Scott C. (US); Borowski, Marianne (US); Kinoshita, Carol (US)
GTAACTCAGATGGCCCTCTGGGCTATCATGGCTGCTCCTTTATTCATGTCTAATGACCTC
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CS135670.1 GI:72056330

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1 (bases 1 to 1290)
Garger, S.J., Turpen, T.H. and Kumagai, M.H.
Production of lygosomal enzymes in plants by transient expression
Patent: US 6887696-A3 03-MAY-2005,
Large Scale Biology Corporation; Vacaville, CA
Location/Qualifiers
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AR653692

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Unclassified.
In (bases 1 to 1290)
I (bases 1 to 1290)
Garger, S.J., Turpen, T.H. and Kumagai, M.H.
Garger, S.J., Typsosomal enzymes in plants by transient expression Patent: US 6890748-A 3 10-MAY-2005;
Large Scale Biology Corporation; Vacaville, CA
Location/Qualifiers
                                                                                                                                          SerileLeuAspTrpThrSerPheAsnGlnGluArgIleValAspValAlaGlyProGly
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Sequence 3 from patent US 6890748.
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/note="Vector: pDNR-Dual" 1.1290	Alignment Scores: 1.37e-207 Length: 1290 Pred. No.: 2314.00 Matches: 421 Score: 2314.00 Matches: 421 Percent Similarity: 100.004 Conservative: 0 Best Local Similarity: 100.004 Mismatches: 0 Query Match: 8 Indels: 0 DB: 8 Gaps: 0	1 MetGlnLeuArgAsnProGluLeu 1 MetGlnLeuArgAsnProGluLeu 1 ATGCAGCTGAGGAACCCAGAACTA 21 LeuValSerTrpAspIleProGly 61 CTCGTTTCCTGGGAACANCCTGGGAA	41 ThrMetGlyTrpLeuHisTrpGluArgPheMetCysAsnLeuAspCysGlnGluBro	81 TrpLysAspalaGlyTyrGluTyrLeuCysIleAspAspCysTrpMetAlaProGlnArg	Qy 101 AspSerGluGlyArgLeuGlnAlaAspProGlnArgPheProHisGlyIleArgGlnLeu 120 Db 301 GATTCAGAACTTCAGGCAGCCCTCAGGGCTTTCCTCATGGGATTCGCCAGCTA 360 Qy 121 AlaAsnTyrValHisSerLy8GlyLeuLy8LeuGlyIleTyrAlaAspValGlyAsnLy8 140 Db 361 GCTAATTATGTTCACAGCAAAGGACTGAAGCATTTATGCAGAATAAA 420	Oy 141 ThrCysalaGlyPheProGlySerPheGlyTyrTyrAspIleAspAlaGlnThrPheAla 160	Qy 181 AlaAspGlyTyrLy8Hi8MetSerLeuAlaLeuAsnArgThrGlyArgSerIleValTyr 200 bb 541 GCAGATGGTTATAAGCACATGTCCTTGGCCCTGAATAGGAGATGGTATAC 600 Qy 201 SerCy8GluTrpProLeuTyrMetTrpProPheGlnLy8ProAsnTyrThrGluIleArg 220 bb 601 TCCTGTGAGTGGCCTCTTTATATGTGGCCCTTTCAAAAGCCCAATTATAGAAATCCGA 660	Oy 221 GlnTyrCygAgnHigTrpArgAsnPheAlaAspIleAgpAgpSerTrplygSerIleLyg 240
Oy 301 ArgHistleSerProGlnAlaLysAlaLeuLeuGlnAspLysAspVall1eAla1leAsn 320	Qy 381 AlaCysPheIleThrGinLeuLeuProValLysArgLysLeuGlyPheTyrGluTrpThr 400 Db 1141 GCCTGCTTCATCACACACCTCCTCCTGTGAAAGGAAGCTAGGGTTCTATGAATGGACT 1200 Qy 401 SerArgLeuArgSerHisIleAsnProThrGlyThrValLeuLeuGlnLeuGluAsnThr 420 Db 1201 TCAAGGTTAAGAAGTCACATAAATCCCACAGGCACTGTTTTGCTTCAGCTAGAAAACCA 1260 Ov 421 Met 421	12 SULT 10 006864 CUS FINITION	_	AUTHORS Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M. and Farmer, A. TITLE Cloning of human full-length CDSs in BD Creator (TM) System Donor	Vector JOURNAL Unpublished REFERENCE 2 (bases 1 to 1290) AUTHORS Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Phelan,M. and Farmer,A. TITLE Direct Submission JOURNAL Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow	Circle, Palo Alto, CA 94303, USA COMMENT This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In Fusion (TM) cloning system between the Sall and HindIII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after Sall site	and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before Hindill site to maintain reading frame. Clone distribution: http://bioinfo.clontech.com/orfclones. Location/Qualifiers 1. 1290 1. 1290 Anglam="Hono sapiens" //db_xref="taxon:9606"	/clone="GHO0112X1.0" /clone lib="BD Creator(TM) CDS Library derived from MGC collection" /lab_host="DH5alpha Tl resistant"

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Matches:
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S. Hines, L., Rolfs, A., Jopson, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Rolfs, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J. and LaBar, J.

Direct Submission
Direct Submission
Submitted (04-JAN-2005) Biological Chemistry and Molecular pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA
This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics.
This ORF clone has been cloned with normalized stop-codon. The CDS has been directionally cloned using BD In-Fusion(TW) cloning system between the Sall and Hindlil sites of the pDNR-Dual vector.
Additional sequences in the clone: 'ACC' after Sall site and
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Human ORF Project.

Bynthetic construct
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                                                                                                                   GlyTrpAsnAspProAspMetLeuVal11eGlyAsnPheGlyLeuSerTrpAsnGlnGln
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/product="galactosidase alpha"
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DWGVDLLKFDGCYCDSLENLADGYKHMSLALNRTGRSIVYSCEWPLYWWPFQKPNYTE
IRQYCNHWRNPADIDDSWKSIKSILDWTSRNQERIVGSGWNDPDMLVIGNFGLS
WNQCYTQMALWAIMAAPLFMSNDLRHISPQAKALLQDKDVIAINQDPLGKGGYQULRQG
DNFEVWERPLSGLAWAVAMIRQBIGGSRSYTIANASJGKGYACNPACFITQLLPVKR
KLGFYEWTSRLRSHINPTGTVLQLENTMQMSLKDL"
                                                                         Direct Submission
Submitted (04-JAN-2005) Biological Chemistry and Molecular
Submitted (04-JAN-2005) Biological Chemistry and Molecular
Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
Cambridge, MA 02141, USA
This CDS clone is a part of a collection of human full-length
expression clones generated by Harvard Institute of Proteomics.
This ORF clone has been cloned with normalized stop-codon. The CDS
has been directionally cloned using BD In-Fusion(TM) cloning system
between the Sall and HindIII sites of the pDNR-Dual vector.
Additional sequences in the clone: 'ACC' after Sall site and
before 'ATG' to provide Kozak consensus sequence. Each clone is
clonally isolated and full-length sequence-verified.
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Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F.,
Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,
Williamson, J. and Labaer, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="FLH025770.01X"
/lab host="Escherichia coli DH5alpha Tl resistant"
/note="derived from MGC template"
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| Acronise="synthetic construct"
| Mol_type="mRNA"
| db_xref="taxon:32630"
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alpha (GLA) mRNA, complete cds.
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Bynthetic construct
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Synthetic construct Homo sapiens clone FLH025766.01L galactosidase
alpha (GLA) mRNA, partial cds.
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GACTGGGGGGTGTTTGATGTTTGATGTTTGTTACTGTGCACGTTTGGAAAATTTG
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DEFINITION ACCESSION

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Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J. and LaBaer, J.

Niliamson, J. and LaBaer, J.

Direct Submission

L. Submitted (105-JAN-2005) Biological Chemistry and Molecular

Direct Submission

L. Submitted (105-JAN-2005) Biological Chemistry and Molecular

Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,

Cambridge, MA 02141, USA

This CDS clone is a part of a collection of human full-length

expression clones generated by Harvard Institute of Proteomics.

This ORF clone has been cloned without stop-codon (to allow fusion

With C-terminal tag). The CDS has been directionally cloned using

BD In-Fusion(TM) cloning system between the Sall and HindIII sites

of the pDNR-Dual vector. Additional sequences in the clone: 'ACC'

after Sall site and before 'ATG' to provide Kozak consensus

sequence, 'GG' after last codon and before HindIII site to maintain

reading frame. Bach clone is clonally isolated and full-length
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                                                                                                                Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J. and LaBaer, J.
Cloning of human full-length CDS in Creator (TM) recombinational
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Matches:
Conservative:
Mismatches:
Indels:
                                                                             other sequences; artificial sequences.
1 (bases 1 to 1290)
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AX892090.1 GI:60652624
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Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S.,
Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y.,
Roundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y.,
Phelan, M. and Farmer, A.

Direct Submission

M. Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow
Circle, Palo Alto, CA 94303, USA

This CDS clone is a part of a collection of human full length
expression clones generated by BD Biosciences Clontech and the
Harvard Institute of Proteomics. Each CDS has been cloned in two
forms: with and without stop-codon (to allow fusion with C-terminal
tag). The CDS has been directionally cloned using BD In-Fusion(TM)
cloning system between the Sall and HindIII sites of the pDNR-DUAL
vector. Additional sequences in the clone: 'ACC' after Sall site
and before 'ATG' to provide Kozak consensus sequence; 'GG' after
last codon and before HindIII site to maintain reading frame.
Clone distribution: http://bioinfo.clontech.com/orfclones.
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IROYCNHWRNFADIDDSWKSIKSILDWTSRNQERT VDVAGFGGWNDPDMLVIGNFGLS
WNGOYTQMAALWAIMAAPLEWBNDLRHIS PQAKALLQDKDVIAINQDPLGKQGYQLRGL
WNGOYTQMRERELSGRAVAMINRQBIGGPRGYIAANASLGKGVACNPACFITGLLPVKR
KLGFYEWTSRLRSHINPTGTVLLQLENTWQMSLKDLLL"
                                                                                                                                                                                                                                                                                                                                                                                                                           other sequences; artificial sequences.
1 (bases 1 to 1290)
Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /trānslation="MOLRNPELHLGCALALRPLALVSWDIPGARALDNGLARTPTWGW
LHWBRFWCNLDCQEEPDSCISEKLFWEMAELMVSEGWKDAGYEYLCIDDCWMAPQRDS
EGRLQADPQRFPHGIRQLANYVHSKGLKLGIYADVGNKTCAGFPGSFGYYDIDAQTFA
                                                          1201 TCAAGGTTAAGAAGTCACATAAATCCCACAGGCACTGTTTTGCTTCAGCTAGAAATACA 1260
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construct Homo sapiens galactosidase, alpha mRNA, partial
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| trans] table=11
|product="Homo sapiens galactosidase, alpha"
| protein id="AAP36507.1"
| db_xref="GI:30584589"
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/note="Vector: pDNR-Dual"
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/mol_type="mRNA"
/db_xref="taxon:32630"
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	401 1201 421 1261 SULT 15	ITION Sequence 9 from patent US 6887696. SION AR653695. ON AR653695.1 GI:67584280 E Unknown. ANISM Unknown. ANISM Unknown. ENER I (bases I to 1296) ENER I (bases I to 1296) HORS Garger, S.J., Turpen, T.H. and Kumagai, M.H.	TITLE Production of lysosomal enzymes in plants by transient expression JOURNL Patent: US 6887696-4 9 03-MAY-2005; Large Scale Biology Corporation; Vacaville, CA EATURES Location/Qualifiers 1. 1296 /organism="unknown" /mol_type="genomic DNA"	Alignment Scores: 1.38e-207 Length: 1296 Pred. No.: 2314.00 Matches: 421 Score: 100.00\$ Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 6 Gaps: 0	US-10-602-219-12 (1-421) x AR653695 (1-1296) QY	61 CTGTTTCCTGGGACCTCCTGGGGCTTGGACTGGATTGGATTGGCAAGGCCTCTCGCTTTTTTTT	Qy 61 AspSerCysIleSerGluLysLeuPheMetGluMetAlaGluLeuMetValSerGluGly 80
rcent Similarity: 100.00% Conservative: 0 st Local Similarity: 100.00% Mismatches: 0 ery Match: 100.00% Mismatches: 0 ery Match: 100.00% Mismatches: 0 in Gaps: 0 -10-602-219-12 (1-421) x BT007835 (1-1290) 1 MetGlnLeuArgAsnProGluLeuHisLeuGlyCysAlaLeuAlaLeuArgPheLeuAla	Db 61 CTGGTTTCCTGGGACATCCTGGGGCTAGAGCACTGGACAATGGATTGGCAAGGACGCT 120	Db 241 TGGAAGGATGCAGGTTATGAGTACCTCTGCATTGATGATGGCTCCCCAAAGA 300 Cy 101 AspSerGluGlyArgLeuGlnAlaAspProGlnArgPheProHisGlyIleArgGlnLeu 120 Cy 101 AspSerGluGlyArgLeuGlnAlaAspProGlnArgPheProHisGlyIleTITIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ThrCysAlaGlyPheProGlySerPheGlyTyrTyrAspIleAspAlaGlnThrP	Oy 181 AlaAspGlyTyrLysHisNetSerLeuAlaLeuAsnargThrGlyArgSerIleValTyr 200	Qy 221 GlnTyrCysAsnHisTrpArgAsnPheAlaAspIleAspAspSerTrpLysSerIleLys 240 Db 661 CAGTACTGCAAATCTTGCTGACATTGATGATCCTGGAAAAGTATAAAG 720 Qy 241 SerIleLeuAspTrpThrSerPheAsnGlnGluArgIleValAspValAlaGlyProGly 260 Db 721 AGTATCTTGGACTGGACATCTTTTAACCAGGAGAAATTGTTGATGTTGCTGGACCAGGG 780	261 GlyTrpAsnAspProAspMetLeuVallleGlyAsnPheGlyLeuSerTrpAsnGlnGln 11	Db 841 GTAACTCAGATGGCCCTCTGGGCTATCATGCTGCTCCTTTATTCATGTCTAATGACCTC 900 Qy 301 ArgHisIleSerProGlnAlaLysAlaLeuLeuGlnAspLysAspVallleAlaIleAsn 320

AspSerGluGlyArgLeuGlnAlaAspProGlnArgPheProHisGlylleArgGlnLeu 120 	. AlaabntyrvalhisSerLygGlyLeuLygLeuGlyIleTyrAlaabpvalGlyAsnLyg 140 	ThrcysalaglyPheProglySerPheGlyTyrTyrAsplleAspAlaglnThrPheAla	AspirpGlyValaspieuleulysPheaspGlyCysTyrCysAspSerLeuGluAsnieu 180 	. AlaaspglytytlyshismetSerleualaleuasnargthrglyargSerileValTyr 200 	SercysGluTrpProLeuTyrMetTrpProPheGlnLysProAsnTyrThrGluIleArg 220 	GINTYrCysabnHisTrpargasnPhealaaspileaspaspserTrpLysSerIleLys 240	SetileLeuaspTrpThrSerPheAsnGlnGluarglleValaspValAlaGlyProGly 260	GlyTrpAsnaspProAspMetLeuVallleGlyAsnPheGlyLeuSerTrpAsnGlnGln 280 	ValThrGlnMetAlaLeuTrpAlaIleMetAlaAlaProLeuPheMetSerAsnAspLeu 300 	301 ArgHislleSerProGlnAlaLysAlaLeuLeuGlnAspLysAspVallleAlaIleAsn 320 	GlnaspprobeuglybysglnglyfyrglnbeuargglnglyaspasnphegluvalTrp 340 	GlubrgProbeuSerGlyLeualaTrpAlaValalaWetileAsnbrgGlnGluileGly 360 	GlyprokrgSerTyrThrIleAlaValAlaSerLeuGlyLysGlyValAlaCysAsnPro 380 	AlacysPheileThrGlnLeuLeuProValLysArgLysLeuGlyPheTyrGluTrpThr 400 	SerargleuargSerHislleasnProThrGlyThrValLeuLeuGlnLeuGluasnThr 420 	Met 421 ATG 1263
AspSerG GATTCAG	AlaAsnT GCTAATT	Thrcysa accrece	AspTrpG GACTGGG	AlaAspG GCAGATG	SerCysG TCCTGTG	GlnTyrC CAGTACT	SerileL AGTATCT	GlyTrpA GGTTGGA	valThrG GTAACTC	Arghisi CGACACA	GlnAspP CAGGACC	GluargP GAACGAC	GlyProa GGACCTO	AlaCysP GCCTGCT	SerArgL TCAAGGT	Met 421 amg 126
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Sequence 20, Appli Sequence 6, Appli Sequence 6, Appli Sequence 4, Appli Sequence 3, Appli Sequence 26, Appli Sequence 1, Appli Sequence 26, Appli Sequence 202, Appli Sequence 9, Appli Sequence 10, Appli Sequence 10, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli

ALIGNMENTS

Sequence 12, Application US/08993059;
Patent No. 6887696;
GENERAL INPORMATION:
APPLICANT: GARGER, Thomas H.
APPLICANT: TURPEN, Thomas H.
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION:
TITLE OF INVENTION NUMBER: US/09/993,059;
CURRENT FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
; SOFTWARRE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12. US-09-993-059-12

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trype: PRT CRGANISM: Homo sapiens US-09-993-059-12

Gaps ô Length 421; Indels Score 2314; DB 2; Pred. No. 1.4e-234; ; Mismatches 0; ö 100.0%; Conservative Similarity 421; Query Match Best Local Best Loca Matches

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9 9 1 MQLRNPELHIGCALAIRFLALVSWDIPGARALDNGLARTPTWGWLHWERFWCNLDCQEEP MQLRNPELHLGCALALRFLALVSWDIPGARALDNGLARTPTMGWLHWERFMCNLDCQEEP н

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US-10-602-219-12 2314 1 MQLRNPELHLGCALALRFLA......RIRSHINPTGTVLLQLENTM 421 score: Sequence: Title: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

572060 Total number of hits satisfying chosen parameters: 572060 segs, 82675679 residues Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries seq length: 0 seq length: 2000000000 8 0 0 0 Minimum Maximum M

Patents_AA:* Issued Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ADGYKHMSLALNRTGRSIVYSCEWPLYMWPPQKPNYTEIRQYCNHWRNFADIDDSWKSIK 240
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                                                                                                                                            Sequence 12, Application US/10103327

Patent No. 6890748

GENERAL INPORMATION:
APPLICANT: GARGER, Stephen A.
APPLICANT: TURREN, Thomas H.
APPLICANT: KTWAGAI, Monto H.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
CURRENT APPLICATION NUMBER: US/09/993,059
PRIOR APPLICATION NUMBER: US/09/993,059
PRIOR APPLICATION NUMBER: US/09/993,059
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 421
TYPE: PRT
CREANISM: Homo sapiens
US-10-103-327-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 2314; DB 2;
100.0%; Pred. No. 1.4e-234;
tive 0; Mismatches 0;
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Patent No. 6887696
GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 421; Conservative
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US-09-993-059-14
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US-10-103-327-12
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APPLICANT: GARGER, Stephen A.
APPLICANT: TURBEN, Thomas H.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
FILE REFERENCE: 008010087CPUS06
CURRENT APPLICATION NUMBER: US/09/993,059
CURRENT APPLICATION NUMBER: US/09/993,059
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 14
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Patent No. 6890748

GENERAL INFORMATION:

APPLICANT: GARGER, Stephen A.

APPLICANT: TUREEN, Thomas H.

APPLICANT: KUMAGAI, Monto H.

TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN

TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN

TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN

FILE REFERENCE: 008010087CPUS06

CURRENT APPLICATION NUMBER: US/10/103,327

CURRENT APPLICATION NUMBER: US/09/993,059

PRIOR FILING DATE: 2001-11-13

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 427
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100.0%; Pred. No. 1.5e-234;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 421; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/602,608
                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e-234;
Matches 421; Conservative 0; Mismatches 0;
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 429 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                MOLECULE TYPE: protein US-07-602-824A-2
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                                                                                                  Gaps
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GENERAL INFORMATION:
APPLICANT: Desnick, Robert J.
APPLICANT: Lashop, David F.
APPLICANT: Lashop, Vainnis A.
TITLE OF INVENTION: CLONING AND EXPRESSION OF BIOLOGICALLY
TITLE OF INVENTION: ACTIVE alpha-GALACTOSIDASE A
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREE: 1155.Avenue of the Americas
CITY: New York
COMPUTRY: U.S.A.
ILS: Avenue of the Americas
CITY: New York
COMPUTRY: U.S.A.
ILS: Avenue of the Americas
COMPUTRY: ID 36
COMPUTRY: ID 36
COMPUTRY: ID 4036
COMPUTRY: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTRY: APPLICATION DATA:
APPLICATION NUMBER: US/07/602,824A
FILING DATE: 24-OCT-1990
CLASSIFICATION NUMBER: US/07/602,824A
FEFERRENCY/CET NUMBER: 0593-005
TELECOMMUNICATION INDORMATION:
TELEPHONE: (212) 790-9090
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                                                           Query Match 100.0%; Score 2314; DB 2; Length 427; Best Local Similarity 100.0%; Pred. No. 1.5e-234; Matches 421; Conservative 0; Mismatches 0; Indels 0
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 ; ORGANISM: Homo sapiens
US-10-103-327-14
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Patent No. 5382524

GENERAL INFORMATION:

APPLICANT: Besnick, Robert J.

APPLICANT: Bishop, David F.

APPLICANT: Bishop, David F.

APPLICANT: Mannis A.

APPLICANT: Mannis A.

TITLE OF INVENTION: CLONING AND EXPRESSION OF BIOLOGICALLY

TITLE OF INVENTION: ACTIVE ALPHA-N-ACETYLGALACTOSAMINIDASE

NUMBER OF SEQUENCES: 24

CORRESPONDENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: PENNIE & EDMONDS

STREET: 1155 Avenue of the Americas
                                               ö
Length 429;
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61 DSCISEKLFMEMAELMVSEGWKDAGYEYLCIDDCWMAPQRDSEGRLQADFQRFFHGIRQL 120
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Sequence 3, Application US/08261578

Patent No. 5491075

APPLICANT: Bishop, David F.

APPLICANT: Lashop, David F.

APPLICANT: Loannou, Yiannis A.

APPLICANT: Mang, Anne M.

TITLE OF INVENTION: CLONING AND EXPRESSION OF BIOLOGICALLY
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                                           COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/983,451
FILING DATE: 30-NOV-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: COLUZZI, LAULER A.
REGISTRATION NUMBER: 6923-030
TELEFRACE/DOCKET NUMBER: 6923-030
TELEFRACE/DOCKET NUMBER: 6923-030
TELEFRACE 212-690-9864/9741
TELEFRACE 212-690-9864/9741
TELEFRACE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 429 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 2314; DB 1; Best Local Similarity 100.0%; Pred. No. 1.5e-234; Matches 421; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-983-451-2
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Fatent No. S401650
Fatent Desnick, Robert J.
FAPLICANT: Bishop, David F.
FAPLICANT: Bishop, David F.
FATILE OF INVENTION: Cloning and Expression of Biologically TITLE OF INVENTION: Cloning and Expression of Biologically TITLE OF INVENTION: Active alpha-Galactosidase A.
FATILE OF INVENTION: Activ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 2314; DB 1; Length
Pred. No. 1.5e-234;
0; Mismatches 0; Indels
FILING DATE: 24-OCT-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COCTUZI, LBUTE A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 623-008
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 790-990
TELEFAX: (6141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CRARACTERISTICS:
LENGTH: 429 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: unknown.1
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Best Local Similarity 100.0%;
Matches 421; Conservative 0
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MOLECULE TYPE: protein
US-07-602-608-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 ADGYKHMSLALNRTGRSIVYSCEWPLYMWPFQKPNYTEIRQYCNHWRNFADIDDSWKSIK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 ADGYKHMSLALINRTGRSIVYSCEWPLYMWPFQKPNYTEIRQYCNHWRNFADIDDSWKSIK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SILDWTSFNQERIVDVAGPGGWNDPDMLVIGNFGLSWNQQVTQMALWAIMAAPLFMSNDL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RHISPOAKALLODKDVIAINODPLGKQGYQLRQGDNFEVWERPLSGLAWAVAMINRQEIG 360
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ACTIVE ALPHA-N-ACETYLGALACTOSAMINIDASE
                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,578
FILING DATE: 17-70N-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/602,608
FILING DATE: 24-0CT-1990
ATTORNEY/AGENT INFORMATION:
NAME: COPLEXI, Laura A.
                                                               STREET: 1155 Avenue of the Americas CITY: New York STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                      NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-008
                                                                                                                                ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
            NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 429 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 421; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / MOLECULE TYPE: protein
US-08-261-578-3
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Best Local Similarity
 TITLE OF INVENTION:
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61 DSCISEKLFMEMAELMVSEGWKDAGYEYLCIDDCWMAPQRDSEGRLQADPQRFPHGIRQL 120
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                                                                       APPLICANT: Desnick, Robert J.
APPLICANT: Bishop, David F.
APPLICANT: Doannou, Yiannis B.
TITLE OF INVENTION: Cloning and Expression of Biologically
TITLE OF INVENTION: Active alpha-Galactosidase A
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,577
FILING DATE: 17-701-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LBUTA A.
REFERENCE/DOCKET NUMBER: 6923-042
REFERENCE/DOCKET NUMBER: 6923-042
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 2314; DB 1;
100.0%; Pred. No. 1.5e-234;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                           ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
; Sequence 7, Application US/08261577; Patent No. 5580757; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
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Matches 421; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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GPRSYTIAVASLGKGVACNPACFITQLLPVKRKLGFYEWTSRLRSHINPTGTVLLQLENT 420
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RHISPQAKALLODKDVIAINODPLGKOGYOLROGDNFEVWERPLSGLAWAVAMINROBIG 360
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                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/09993059;
Patent No. 6887696;
GENERAL INFORMATION:
APPLICANT: GARGER, Stephen A.;
APPLICANT: TUREN, Thomas H.
APPLICANT: KUNAGAI, Monto H.
TILLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN TILLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION: TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION: FILE REFERENCE: 008010087CPUS06; CURRENT APPLICATION NUMBER: US/09/993,059; CURRENT APPLICATION NUMBER: 2001-11-13; NUMBER OF SEQ ID NOS: 37; SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.
Matches 421; Conservative
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US-09-993-059-10
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                     361 GPRSYTIAVASLGKGVACNPACPITOLLPVKRKLGFYEWTSRLRSHINPTGTVLLOLENT 420
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                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Desnick, Robert J.
APPLICANT: Bishop, David F.
APPLICANT: Sishop, David F.
APPLICANT: Icannou, Yiannis A.
TITLE OF INVENTION: Cloning and Expression of Biologically
TITLE OF INVENTION: Active alpha-Galactosidase A
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPOTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,577
FILING DATE: 17-UN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COPICAZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-042
TELECPMONINICATION: 1900-9090
TELECPMONINICATION: 1900-9090
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Pred. No. 1.5e-234;
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STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                             Sequence 9, Application US/08261577
Patent No. 5580757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212) 869-8864
TELEX: 66141 PENNIB
INPORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 429 amino acids
TYPE: amino acid
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Best Local Similarity 100.
Matches 421; Conservative
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180

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121 ANYVHSKGLKLGIYADVGNKTCAGFPGSFGYYDIDAQTFADWGVDLLKFDGCYCDSLENL 180
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US-10-103-327-6

Sequence 6, Application US/10103327

Sequence 6, Application US/10103327

Patent No. 6890748

GENERAL INFORMATION:

APPLICANT: GARGER, Stephen A.

APPLICANT: TURPEN, Thomas H.

APPLICANT: TURBATION: PRODUCTION OF LYSOSOMAL ENZYMES IN TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION FILE REFERENCE: 008010087CPUS06

CURRENT APPLICATION NUMBER: US/10/103,327

CURRENT APPLICATION NUMBER: US/09/993,059

PRIOR PILING DATE: 2002-03-20

PRIOR PILING DATE: 2001-11-13
                                                                                                                                                                                                 100.0%; Score 2314; DB 2;
100.0%; Pred. No. 1.5e-234;
ive 0; Mismatches 0;
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illarity 100.0%; Pred. No. 1.5e-234;
Conservative 0; Mismatches 0;
CURRENT FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 37
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 6
                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 421; Conservative
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-327-6
                                                                                      ; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-993-059-6
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Best Local Similarity
Matches 421; Conserv
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                                                          Sequence 10, Application US/10103327

Patent No. 6890748

GENERAL INPORMATION:
APPLICANT: GARGER, Stephen A.
APPLICANT: TURPEN, Thomas H.
APPLICANT: KUMAGAI, Monto H.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
CURRENT FILING DATE: 2002-03-20
PRIOR PILING DATE: 2002-03-20
PRIOR FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0

SECTION OF SEQ ID NOS: 37
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Patent No. 6887696
GENERAL INFORMATION:
APPLICANT: GARGER, Stephen A.
APPLICANT: TURPER, Thomas H.
APPLICANT: KUMAGAI, Monto H.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
FILE REPERSENCE: 008010087CFUS06
CURRENT APPLICATION NUMBER: US/09/993,059
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100.0%; Pred. No. 1.5e-234;
tive 0; Mismatches 0;
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Matches 421; Conservative
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ORGANISM: Homo sapiens
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SEQUENCE CHARACTERISTICS
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CELL TYPE:
CELL LINE:
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                      1 MQLRNPELHIGCALALRFLALVSWDIPGARALDNGLARTPTWGWLHWERFWCNLDCQEEP
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MQLRNPELHLGCALALRFLALVSWDIPGARALDNGLARTPTMGWLHWERFMCNLDCQEEP
                                                                                     DSCISEKLFMEMAELMVSEGWKDAGYEYLCIDDCWMAPQRDSEGRLQADPQRFPHGIRQL
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09070356

Sequence 4, Application US/09070356

Patent No. 6228631

SENERAL INFORMATION:

APPLICANT: Alex Substance

TITLE OF INVENTION: Recombinant a-N-
TITLE OF INVENTION: Acety1galactosaminidase
TITLE OF INVENTION: Acety1galactosaminidase
TITLE OF INVENTION: Said Enzyme
CORRESPONDENCES: 7

CORRESPONDENCES: 7

COUNTRY: U.S.A.

ZIP: 10016

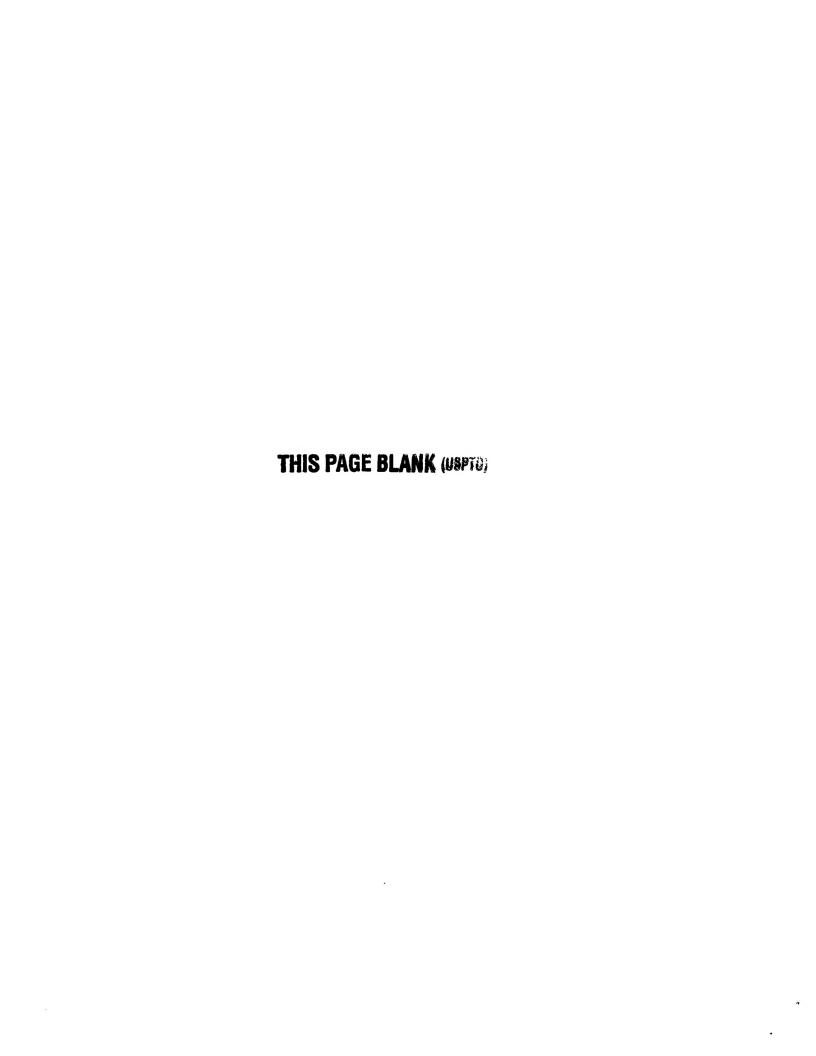
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 08/037,248
FILING DATE: March 26, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 43,494
REFERENCE/DOCKET NUMBER: 63475/12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
TELEPHONE: (212) 286-0854 or 286-0082
TELEPHONE: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 4:
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US-09-070-356-4
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181 ADGYKHMSLALNRTGRSIVYSCEWPLYMWPFOKPNYTFIRQYCNHWRNFADIDDSWKSIK 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: Cahloun et al
AUTHORS: Cahloun et al
TITLE: Rabry Disease: Isolation of a CDNA
TITLE: Pabry Disease:
JOURNAL: Proceedings of the National Academy
VOLUME: 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.8%; Score 2310; DB 2; 99.0%; Pred. No. 3.9e-234; ative 4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: human a-galactosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                              to mRNA
                                                                                                                                                                                                                                                                                                                                                        library
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Best Local Similarity 99.0
Matches 417; Conservative
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IMMEDIATE SOURCE: 11bb
POSITION IN GENOME: un
CHROMOSOME/SEGMENT:
NAP POSITION:
UNITS:
FEATURE:
                                                                                                                                                                                                                  INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
TYPE: amino acid
STRANDEDNESS: dout
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: CDNA
HYPOTHETICAL: no
                                                                            CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 82
7364-7368
                                                                                                                 ANTI-SENSE: yes
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: human
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421 M 421 | 421 M 421

Search completed: December 24, 2005, 09:12:00 Job time : 45 secs

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                  Copyright
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- protein search, using sw model OM protein December 24, 2005, 09:07:49 Run on:

; Search time 40 Seconds (without alignments)
1012.681 Million cell updates/sec

US-10-602-219-12 Perfect score:

1 MQLRNPELHLGCALALRFLA......RLRSHINPTGTVLLQLENTM 421 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

seq length: 0 seq length: 200000000 88 Minimum | Maximum |

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
7	2314	100.0	429	П	двния	alpha-galactosid
7	1811	78.3	419	~	JC4522	alpha-galactosid
٣	1051	45.4	405	~	S45522	alpha-N-acetylga
4	952.5	41.2	411	~	A35485	alpha-N-acetylga
S	930	40.2	358	~	A33265	alpha-N-acetylga
9	862	37.3	451	~	T24018	hypothetical pro
7	716.5	31.0	434	~	T47748	alpha-galactosid
80	712	30.8	378	~	T50781	alpha-galactosid
თ	687.5	29.7	422	~	T06388	alpha-galactosid
10	682	29.5	425	~	T10860	alpha-galactosid
11	681.5	29.5	411	~	S07472	alpha-galactosid
12	919	29.5	680	~	T36472	probable secrete
13	609	26.3	436	~	T39118	probable alpha-g
14	598	25.8	396	~	JC5558	alpha-galactosid
. 15	557	24.1	469	~	S45453	alpha-galactosid
16	543.5	23.5	545	~	\$23582	alpha-galactosid
17	521	22.5	471	~	S50312	alpha-galactosid
18	519	22.4	471	~	S50311	alpha-galactosid
19	516	22.3	444	~	S74221	alpha-galactosid
20	514	22.2	471	~	JQ1021	alpha-galactosid
21	510	22.0	471	~	S50310	alpha-galactosid
22	502	21.7	471	-	GBBYAG	alpha-galactosid
23	300.5	13.0	204	N	T04423	probable alpha-g
24	282.5	12.2	432	~	F83883	hypothetical pro
25	198	9.8	159	~	T04422	alpha-galactosid
26	180.5	7.8	624	~	S74222	alpha-galactosid
27	129	5.6	641	~	A55549	glucan 1,6-alpha
28	125	5.4	4	~	03	hypothetical pro
29	116	5.0	4199	~	S76412	

alpha-amylase (EC	alpha-galactosidas hypothetical prote	hypothetical prote	Subtilase family p	alpha-amylase (imp	hypothetical prote	alpha-galactosidas	cellulase - Cellul	transglycosylase,	alpha-amylase (EC	alpha-amylase (EC	N-acetylgalactosam	ATP synthase subun	hypothetical prote	hypothetical prote	
S14957	S44254 D90496	T35882	AI2007	C86781	T36462	A43717	S49541	E87414	S14956	T02956	KJHUAB	H90202	E85062	T19442	
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114.5	114	106.5	103.5	103	101.5	100.5	99.5	96	97.5	96	95.5	93	93	92.5	
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Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cibace: 30-Jun-1987 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004
Cibacession: S04081; A29608; A30214; S14879; A00896; B00896; I37140
R;Kornreich, R.; Desnick, R.J.; Bishop, D.F.
Nucled: Adids Res. 17, 3302, 1989
A;Title: Nucleotide sequence of the human alpha-galactosidase A gene.
A;Reference number: S04081; MUID:89263745; PMID:2542896 N;Alternate names: alpha-D-galactoside galactohydrolase; melibiase

A; Accession: S04081

A; Status: translation not shown
A; Molecule type: DNA
A; Cross-references: UNIPROT: P06280; UNIPARC: UPI0000033A30; EMBL:X14448; NID:g31755; PIDN
R; Quinn, M.; Hantzopoulos, P.; Fidanza, V.; Calhoun, D.H.
A; Quinn, M.; Hantzopoulos, P.; Fidanza, V.; Calhoun, D.H.
A; Title: A genomic clone containing the promoter for the gene encoding the human lysosom
A; Reference number: A29608; MUID:88112869; PMID:2892762

A; Accession: A29608

A; Molecule type: DNA A; Residues: 1-64 <QUI>

A,Gross-references: UNIPARC:UPI000016A96A; GB:M18242; NID:g182944; PIDN:AAA52514.1; PID R;Bishop, D.F.; Kornreich, R.; Desnick, R.J.
Proc. Natl. Acad. Sci. U.S.A. 85, 3903-3907, 1988
A;fitle: Structural organization of the human alpha-galactosidase A gene: further eviden A;Reference number: A30214; MUID:88234528; PMID:2836863

A;Accession: A30214

A; Molecule type: DNA A; Residues: 1-64 <BIS>

A;Cross-references: UNIPARC:UPI000016A96A; EMBL:M20317; EMBL:J03249
R;Koide, T.; Ishiura, M.; Iwai, K.; Inoue, M.; Kaneda, Y.; Okada, Y.; Uchida, T.
R;Koide, T.; Ishiura, M.; Iwai, K.; Inoue, M.; Kaneda, Y.; Okada, Y.; Uchida, T.
BESS Lett. 259, 353-356, 1990
A;Title: acse of Fabry's disease in a patient with no alpha-galactosidase A activity of A;Reference number: 314879
A;Reference number: 314879
A;Rocession: S14879
A;Molecule type: mRNA
A;Residues: 1, K., 3-39, S., 41-429 <KOI>A;Residues: 1, K., 3-39, S., 41-429 EMBL:X16889

A;Experimental source: Fabry's disease patient.
R;Bishop, D.F.; Calhoun, D.H.; Bernstein, H.S.; Hantzopoulos, P.; Quinn, M.; Desnick, R. Proc. Natl. Acad. Sci. U.S.A. 83, 4869-4863, 1986
A;Title: Human alpha-galactosidase A: nucleotide sequence of a cDNA clone encoding the paymeterence number: A00896; MUID:86259694; PMID:3014515

A;Molecule type: mRNA *Residues: 27-429 <BL2> A;Crose-references: UNIPARC:UPI000000358; GB:M13571; NID:g178245; PIDN:AAA51676.1; PID A;Experimental source: lung

A,Accession: B00896 A,Molecule type: protein

PIDN

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A; Residues: 32-55,'S',57-58,'R',60-65,'S',67-68;228-332,'N',234-237,'A';298-326;'L',334-A;Cross-references: UNIPARC:UPI00001729C6; R;Tsul', S.; Martin, B.M.; Kaslow, D.C.; Migeon, B.R.; Choudary, P.V.; Stubblefiled, B.R. Eur. J. Blochem. 165, 275-280, 1987
A; Title: Signal sequence and DNA-mediated expression of human lysosomal alpha-galactosic A;Recence number: 137140; MUID:87246603; PMID:3036D6
A;Recidues: 1-429 e.RES
A;Cross-references: UNIPARC:UPI0000033A30; EMBL:X05790; NID:g28535; PIDN:CAA29232.1; PID
A;Residues: 1-429 e.RES
A;Cross-references: UNIPARC:UPI000033A30; EMBL:X05790; NID:g28535; PIDN:CAA29232.1; PID
A;Residues: 1-429 e.RES
A;Cross-references: GDB:119272; OMIM:301500
A;Map position: KQ21.3-KQ22
A;Introns: 65/2; 123/3; 183/1; 213/3; 267/3; 333/3
C;Superfamily: alpha-galactosidase
C;Keywords: Fabry disease; Glycolipid metabolism; glycoprotein; glycosidase; hydrolase; F;1-31/Domain: signal sequence #status predicted <RIC
F;1-31/Domain: signal sequence #status predicted <AMI>F;1-40/Pomain: signal sequence #status predicted <AMI>F;1-39,192,215,408/Binding site: carbohydrate (Asn) (covalent) #status predicted
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alpha-galactosidase (EC 3.2.1.22) A precursor - mouse

alpha-galactosidase (EC 3.2.1.22) A precursor - mouse

N.Alternate names: alpha-D-galactoside galactohydrolase
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: JG4522
R;Ohshima, T.; Murray, G.J.; Nagle, J.W.; Quirk, J.M.; Kraus, M.H.; Barton, N.W.; Brady, A;Accession: JG4522
A;Attle: Structural Organization and expression of the mouse gene encoding alpha-galactc
A;Reference number: JG4522; MUD:96125203; PMID:8543175
A;Accession: JG4522
A;Molecule type: mRNA
A;Residues: 1-419 <OHS>
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C;Species: Gallus gallus (chicken)
C;Species: Gallus (chicken)
C;Species
                                                                  Experimental source: kidney, C57BL Comment: This enzyme is a lysosomal enzyme that hydrolyses the alpha-D-galactosyl
           GB:U34071; NID:g1141787;
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G; Comment: This enzyme is a lysosomal enzyme that hydrolyses the alpha-C; Comment: This enzyme is a lysosomal enzyme that hydrolyses the alpha-C; Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
C;Cenetics:
A;Genetics:
A;Ge
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; Pred. No. 3.2e-82;
58; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 1811; DB 2;
; Pred. No. 2.3e-147;
41; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: nucleic acid
A;Residues: 1-161, A',163-465 <DA2>
A;Crosa: references: UNIPARC:UPI000146A75; GB:L18754
C;Superfamily: alpha-galactosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.3%;
78.2%;
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Best Local Similarity 53.0%;
Matches 206; Conservative 56
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Matches 327; Conservative
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A;Cross-references: UNIPARC:UP10000175B1E; GB:M59199; NID:g1513066; PIDN:AAB06718.1; PID A;Note: sequence extracted from NCBI backbone and corrected to correspond with the trans C;Genetics:
A;Genetics:
A;Gene: GDB:NAGA
A;Cross-references: GDB:119445; OMIM:104170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1990 #sequence_revision 21-Feb-1990 #text_change 09-Jul-2004
C;Accession: A33265
R;Tsuji, S.; Yamauchi, T.; Hiraiwa, M.; Isobe, T.; Okuyama, T.; Sakimura, K.; Takahashi, Biochem. Biochem. Biophys. Res. Commun. 163, 1498-1504, 1989
A;Title: Molecular cloning of a full-length cDNA for human alpha-N-acetylgalactosaminida A;Reference number: A33265; MUID:89392067; PMID:2551294
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A;Introns: 6/1; 51/2; 108/3; 168/1; 199/3; 253/3; 319/3
C;Superfamily: alpha-galactosidase
C;Superfamily: alpha-galactosidase
C;Keywords: alternative splicing; glycoprotein; glycosidase; hydrolase; lysosome
F;1-17/Domain: signal sequence #status predicted <51G>
F;1-17/Domain: signal sequence #status predicted <51G>
                                                                                                                                                                                                                     A;Map position: 22q11-22q11
A;Introns: 6/1; 51/2; 108/3; 168/1; 199/3; 253/3; 319/3; 367/3
A;Introns: 6/1; 51/2; 108/3; 168/1; 199/3; 253/3; 319/3; 367/3
C;Superfamily: alpha-galactosidase
C;Keywords: alternative splicing; glycoprotein; glycosidase; hydrolase; lysosome
F;1-17/Domain: signal sequence #status predicted <SIG>
F;1-17/Domain: aignal sequence #status predicted <NAT>
F;18-411/Product: alpha-N-acetylgalactosaminidase, splice form 2 #status predicted
F;124,177,201,359,385,391/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Cross-references: UNIPROT:P17050; UNIPARC:UPI000016ADB4; GB:M29276; NID:g189052; PIDN
A;Experimental source: clone pcD-H51204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDC#MAPQRDSEGRLQADPQRFPHGIRQLANYVHSKGLKLGIYADVGNKTCAGFPG-SFG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 YYDIDAQTFADWGVDLLKFDGCYCDSLENLADGYKHMSLALNRTGRSIVYSCEWPLYMWP 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 KVVQDAQTFAEWKVDMLKLDGCF-STPEERAQGYPKMAAALNATGRPIAFSCSWPAYEGG 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               330 QL-RQGDNFEVWERPLSGLAWAVAMIN-RQEIGGPRSYTIAVASLGKGVACNPACFITQL 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 LDNGLLQTPPMGWLAWERFRCNINCDEDPKNCISEQLFMEMADRMAQDGWRDMGYTYLNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 F-QKPNYTEIRQYCNHWRNFADIDDSWKSIKSILDWTSFNQERIVDVAGPGGWNDPDMLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 LDNGLARTPTMGWLHWERFMCNLDCQEEPDSCISEKLFMEMAELMVSEGWKDAGYEYLCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 411;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.2%; Score 952.5; DB 2; 50.0%; Pred. No. 9e-74; ive 55; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365 IYEAQDVYSGDIISGLRDETNFTVIINPSGVVMWYL 400
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A,Cross-references: GDB:119445; OMIM:104170
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A;Molecule type: DNA
A;Residues: 1-391 <RES>
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A; Molecule type: mRNA
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Matches 198;
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alpha-N-acetylgalactosaminidase (EC 3.2.1.49) precursor, splice form 2 - human
N;Alternate names: alpha-galactosidase B
C;Species: Homo saplens (man)
C;Species: Homo saplens (man)
C;Date: 31-Aug-1990 #sequence revision 31-Dec-1995 #text_change 09-Jul-2004
C;Accession: A35630; A35648; A37082; I39416
R;Wang, A, M. Bishop, D.F; Desnick, R.J.
J. Biol. Chem. 265, 21859-21866, 1990
A;Title: Human alpha-N-acetylgalactosaminidase-molecular cloning, nucleotide sequence,
                                                                                                                                                                                                 DDCWAAKQRDAEGRIVPDPERFPRGIKALADYVHARGLKLDIYGDLGRLTCGGYPGTTLD 120
                                                                                                                                                                                                                                                                                                                           SUBDAQTFAEWGVDMLKLDGCYSSGKEQ-AQGYPQMARALNSTGRPIVYSCSWPAYQGG 179
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                                                                                                                                                            DDCWMAPQRDSEGRLQADPQRFPHGIRQLANYVHSKGLKLGIYADVGNKTCAGFPG-SFG 150
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                                 91
                                                                180 LPPKVNYTLLGEICKLWRNYDDIQDSWDSVLSIVDWFFTNQDVLQPFAGPGHWNDPDMLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 IGNFGLSYEQSRSQMALWTIMAAPLLMSTDLRTISPSAKKILQNRLMIQINQDPLGIQGR
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Jan 194 ... 14

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A,Map position: 3
A,Introns: 73/2; 93/1; 112/1; 123/3; 158/2; 182/3; 202/2; 224/2; 252/2; 274/1; 301/3; 33
A,Note: F18021.270
C,Superfamily: alpha-galactosidase
                                                                                                                                                                                                                                                                                                     alpha-galactosidase-like protein - Arabidopsis thaliana
N,Alternate names: protein F18021.270
N,Alternate names: protein F18021.270
C;Specias: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47748
S;Benes, V; Wurmbach, B; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Rudd, S.; Lemcke, K.;
Submitted to the Protein Sequence Database, April 2000
A;Reference number: 224474
A;Accession: T47748
A;Accession: T47748
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-434 <BEN>
A;Residues: 1-434 <BEN>
A;Cross-references: UNIPROT:Q9LYL2; UNIPARC:UPI00000A62BB; EMBL:ATF18021
A;Experimental source: cultivar Columbia; BAC clone F18021
91 ETADALVSSGLADLGYIHVNIDDCWSNLLRDSEGQLVPHPETFPSGIKLLADYVHSKGLK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGIYADVGNKTCAGFPGSFGYYDIDAQTFADWGVDLLKFDGCYCDSLENLA----DGYKH 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LD----WISFNQERIVDVAGPGGWNDPDMLVIGNFGLSWNQQVTQMALWAIMAAPLFMSN 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257 ADLNNKWAAY-----AGPGGWNDPDMLEIGNGGWTYEEYRGHFSIWALMKAPLIGC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLRHISPQAKALLQDKDVIAINQDPLGKQGYQLR---QGDNFEVWERPLSGLAWAVAMIN 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alpha-galactosidase (EC 3.2.1.22) [imported] - coffee
C;Species: Coffea arabica (coffee)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C;Accession: TSO781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 GLVFSKSFNSIYDTSMYGRLQLMNGLARTPQMGWNSWNFFACN-----INETVIK
                                                                                              206 MRDALNATGRSIFYSLCEWGVDDPALW-----AKEVGNSWRTTDDINDTWASMTTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKQGYQLRQGDNFEVWER---PLSG--LAWAVAMINRQEIGGPRSYTIAVASLGKGVACN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 GCALALRFLALVSWDIPGARALDNGLARTPTWGWLHWERFMCNLDCQEEPDSCISEKLFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMAELMVSEGWKDAGYBYLCIDDCWMAPQRDSEGRLQADPQRFPHGIRQLANYVHSKGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MSLALNRIGRSIVYS-CEWPL---YMWPFOKPNYTEIRQYCNHWRNFADIDDSWKSIKSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                          PACFITQLLPVKRKLGFYEWTSRLRSHINPTGTVLLQLE 418
                                                                                                                                                                                                    PAGYYVHDIWSHVDLGLLRSGDSIVVSIAPAGSVFFRAD 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 31.0%; Score 716.5; DB 2; Local Similarity 42.4%; Pred. No. 1.7e-53; les 153; Conservative 54; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R 356
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CiSpecies: Caenorhabditis elegans
CiDate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
CiDate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
CiAccession: T24018
RiHarris, B.
Submitted to the EMBL Data Library, July 1996
AiReference number: 219830
AiReference number: 219830
AiReference number: 124018
AiResidues: 124018
AiResidues: 1-451 < WIL>
AiResidues: 1-451 < WIL>
AiResidues: 1-451 < WIL>
AiResidues: 1-651 < WIL>
AiResidues: 1-651 < WIL>
CiGenetics: CiOne R07B7
CiGenetics: CiGenetics: Cone R07B7
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                                                                                                                                                                                                                                                  151 YYDIDAQTFADWGVDLLKFDGCYCDSLENLADGYKHMSLALNRTGRSIVYSCEWPLYMWP 210
                                                                                                                                                                                                                           DDCWMAPQRDSEGRLQADPQRPPHGIRQLANYVHSKGLKLGIYADVGNKTCAGFPG-SFG 150
                                                                                                                                                                                                                                                                                                                                        256 IGNFGLSLEQSRAQMALWTVLAAPLLMSTDLRTISAQNMDILQNPLMIKINQDPLGIQGR 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 SVHIDDCWSEMERDSHGILVANKTRFPSGMKALAKYMHDRGLKPGIYEDYGTKTCGGYPG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 L--IDHPELVNYNLIGKYCNTWRNPDDINSSWKSIISIISYYDKMQDKHIPTHGPGKWHD 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      265 PDMLVIGNFGLSWNQQVTQMALWAIMAAPLFMSNDLRHISPQAKALLQDKDVIAINQDPL 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 GAFCLDNGLGRTPPMGWASWTAFYCEIDCVKHPTGCINEQLYKDMADQLVSGGYDKVGYK 71
                                                                                                                                                                               77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein R07B7.11 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jul-2004
C;Accession: T24018
F;124,177,201/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                        F-QKPNYTEIRQYCNHWRNFADIDDSWKSIKSILDWTSFNQERIVDVAGPGGWNDPDMLV
                                                                                                                                                                                                                                                                                                                                                                                                                                32 LDNGLARTPTMGWLHWERFMCNLDCQEEPDSCISEKLFMEMAELMVSEGWKDAGYEYLCI
                                                                                                                                                             IGNFGLSWNQQVTQMALWAIMAAPLFMSNDLRHISPQAKALLQDKDVIAINQDPLGKQGY
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                                                                                            Gaps
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                                                Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.3%; Score 862; DB 2; Length 45
43.6%; Pred. No. 5.8e-66;
tive 62; Mismatches 149; Indels
                                                                                          Indels
                                           40.2%; Score 930; DB 2; ilarity 57.7%; Pred. No. 6.4e-72; Conservative 40; Mismatches 85
                                                                                          40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Map position: 5;Introns: 61/1; 107/3; 317/3; 351/3; Superfamily: alpha-galactosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 37.3%;
Best Local Similarity 43.6%;
Matches 174; Conservative 6
                                                                Local Similarity
Les 176; Conserv
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RIHKG 320
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alpha-galactosidase (EC 3.2.1.22) - kidney bean
C;Species: Phaseolus vulgaris (Kidney bean)
C;Species: Phaseolus vulgaris (Kidney bean)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10866
R;Davis, M.O.; Walker, J.C.; Smith, D.
submitted to the EMBL Data Library, August 1994
A;Description: Cloning and expression of a pinto bean alpha galactosidase gene.
A;Reference number: Z17189
A;Accession: T10860
A;Accession: T10860
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: mRNA
A;Residues: 1-425 < DAV>
A;Residues: 1-425 < DAV>
A;Cross-references: UNIPROT:Q41100; UNIPARC:UP100000A0F13; EMBL:U12927; NID:g927576; PIC
C;Function:
A;Description: catalyzes hydrolysis of melibiose into galactose and glucose
C;Superfamily: alpha-galactosidase
C;Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                           325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QERIVDVAGPGGWNDPDMLVIGNFGLSWNQQVTQMALWAIMAAPLFMSNDLRHISPQAKA 309
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C;Species: Cyamopsis tetragonoloba (guar, cluster bean)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004
C;Accession: S07472
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                                                        DMLVIGNFGLSWNQQVTQMALWAIMAAPLFMSNDLRHISPQAKALLQDKDVIAINQDPLG
                                                                                                                                                                                                                                                       ||| :|| |: : : ::|: || || : |: || || DMLEVGNGGMTTEEYRAHFSIWSLAKAPLLIGCDIRALDATTKELLSNKEVIAVNQDKLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 MMMSREVDHRRNLVGNGLGQTPPMGWNSWNHFSCN-----INEDLIRETADAMV
                            YYDIDAQTFADWGVDLLKFDGCYCDSLENLADGYKHMSLALNRTGRSIVYS-CEWPLYMW
                                                                                                                             210 PFQKPNYTEIRQYCNHWRNFADIDDSWKSIKSILD----WTSFNQERIVDVAGPGGWNDP
                                                                                                                                                                             --SEDPATWAKSVGNSWRTTGDIQDKWDSMISRADLNDKWASY-----AGPGGWNDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 LALVSWDIPGARAL-DNGLARTPTMGWLHWERFMCNLDCQEEPDSCISEKLFMEMAELMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 425;
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29.5%; Score 682; DB 2; Lv
Best Local Similarity 41.5%; Pred. No. 1.5e-50;
Matches 144; Conservative 54; Mismatches 113;
                                                                                                                                                                                                                                                                                                                         KOGYQLRQGDNFEVWERPLSGLAWAVAMINR 356
                                                                                                                                                                                                                                                                                                                                                           335 VQCKKVKSTNDLEVWAGPLSNNKVAVILWNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha-galactosidase (EC 3.2.1.22) - soybean
C;Species: Glycine max (soybean)
C;Species: Glycine max (soybean)
C;Accession: T06388
R;Davis, M.O.; Walker, J.C.; Smith, D.
submitted to the EMBL Data Library, August 1994
A;Description: Cloning and expression of a soybean alpha galactosidase gene.
A;Reference number: 215645
A;Accession: T06388
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: unipperces: UNIPROT:Q39811; UNIPARC:UP100000A7200; EMBL:U12926; NID:g927574; PID
A;Experimental source: strain williams
C;Function:
A;Description: catalyzes hydrolysis of melibiose into galactose and glucose
C;Superfamily: alpha-galactosidase
C;Keywords: glycosidase; hydrolase
R;Zhu, A.; Goldstein, J.

R;Zhu, A.; Goldstein, J.

A;Title: Cloning and functional expression of a CDNA encoding coffee bean alpha-galactos A;Title: Cloning and functional expression of a CDNA encoding coffee bean alpha-galactos A;Reference number: Z25235; MUID:94193002; PMID:8144030

A;Recension: T50781

A;Status: pre-liminary; translated from GB/EMBL/DDBJ

A;Residues: 1-378 <ZHU>
A;Residues: 1-378 <ZHU>
C;Residues: 1-378 <ZHU

C;Superfamily: alpha-galactosidase

C;Keywords: glycosidase; hydrolase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YYDIDAQTFADWGVDLLKFDGCYCDSLENLADGYKHMSLALNRTGRSIVYS-CEWPLYMW 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 PFQKPNYTEIRQYCNHWRNPADIDDSWKSIKSILD----WTSFNQERIVDVAGPGGWNDP 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DMLVIGNFGLSWNQQVTQMALWAIMAAPLFMSNDLRHISPQAKALLQDKDVIAINQDPLG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||| :|| |: : ::||: || |: |: || DMLEVGNGGMTTTEYRSHPSIWALAKAPLLIGCDIRSMDGATFQLLSNAEVIAVNQDKLG 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 LDNGLGHTPPMGWNSWNHFACN-----IKEDLIRETADAWSTGLAALGYQYINI 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDCWMAPQRDSEGRLQADPQRFPHGIRQLANYVHSKGLKLGIYADVGNKTCA-GFPGSFG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91
                                                                                                                                                                                                                                                                                                                                                                                                                                  LANGLGLTPPMGWNSWNHPRCNLD------EKLIRETADAMVSKGLAALGYKYINL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 VQGNKYKTYGDLEVWAGPLSGKRVAVALWNKGSSTATITAYWSDVGLPSTAVVNARDL 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KOGYQLRQGDNFEVWERPLSGLAWAVAMINR------QEIGGPRSYTIAVASL 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDNGLARTPTMGWLHWERFMCNLDCQEEPDSCISEKLFMEMAELMVSEGWKDAGYEYLCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDNGLARTPTMGWLHWERFMCNLDCQEEPDSCISBKLFMEMAELMVSEGWKDAGYBYLCI
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                                                                                                                                                                                                                                                                                                  Length 378;
                                                                                                                                                                                                                                                                                                Query Match 30.8%; Score 712; DB 2; Length 37 Best Local Similarity 42.5%; Pred. No. 3.4e-53; Matches 152; Conservative 51; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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29.7%; Score 687.5; DB 2;
Best Local Similarity 43.2%; Pred. No. 4.9e-51;
Matches 143; Conservative 45; Mismatches 112;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-436 <HUNA
A;Residues: 1-436 <HUNA
A;Cross-references: UNIPROT:Q9URZO; UNIPARC:UPI000066BE8C; EMBL:AL132779; PIDN:CAB60017.
A;Experimental source: strain 972h-; cosmid c869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 FKFGMYSSAGKYTCAGPPGSLNHEQIDADTFADWGVDYLKYDNCFNEGKSGVPLISYERY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VTOMALWAIMAAPLFMSNDLRHISPQAKALLQDKDVIAINQDPLGKQG----YQLRQGDN 336
                141 FGIYTSAGTKTCSSIGFPGALGHEYSDARQFADWGVDYLKYDNCNNQGVD-AKQRYTTMR 199
                                                                                                            200 DALAATGRPIVYSICEWGENKP---WEWA----GDLGQL---WRTTGDINDSWGSMSSIM 249
                                                                                                                                                                                                        DWTSFNQERIVDVAGPGGWNDPDMLVIGNFGLSWNQQVTQMALWAIMAAPLFMSNDLRHI 303
                                                                                                                                                                                                                                             K---SNLELAEYARPGGWNDPDMLEVGNGGMTDTEYRTHFSWWSIMAAPLLIGTDLRTA 305
                                                                                                                                                                                                                                                                                                                               304 SPQAKALLQDKDVIAINQDPLGKQGYQLRQGDNFEVWERPLSGLAWAVAMINRQEIGGPR 363
                                                                                                                                                                                                                                                                                                                                                                                                    361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYTIAVASLGKGVACNPACFITQLLPVKRKLGFYE-W-----TSRLRSHINPTGTVLL 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 AQRIETTAKAVG------LPKSRGYTWRDLWKHSDTNTTGRIAATVPAHGTVLV 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 MEMAELMVSEGWKDAGYEYLCIDDCWMAPQRD-SEGRLQADPQRFPHGIRQLANYVHSKG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ©;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39118
R;Hunt, C: Aves, S: McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
Bubmitted to the EMBL Data Library, November 1999
A;Reference number: Z21829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKLGIYADVGNKTCAGFPGSFGYYDIDAQTFADWGVDLLKFDGCYCDSLENLA----DGY
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                                                                                                                                                                                                                                                                                                                                                                          | :| : :|||:||||||| : : ||| || || 306 PESAFEILTNDEVIAVDQDPLGKQGEVVSSEGGRWVVSKELADGSRAVALFNE----GSR
                                                                               LALNRIGRSIVYS-CEW----PLYMWPFQKPNYTEIRQYCNHWRNFADIDDSWKSIKSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable alpha-galactosidase - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.3%; Score 609; DB 2; Length 43
35.8%; Pred. No. 2.7e-44;
tive 65; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F-EVWERPLSGLAWAVAMIN 355
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Matches 136; Conservative
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RV 411
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C;Superfamily: a
                                                                                                                                                                                                               244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable secreted alpha-galactosidase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36472
R;Seeger, K.J.; Harris, D.; Thomson, N.R.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
R;Seeger, K.J.; Harris, Data Library, September 1999
A;Accession: T36472
A;Accession: T36472
A;Accession: Preliminary; translated from GB/EMBL/DDBJ
A;Accession: Preliminary; translated from GB/EMBL/DDBJ
A;Accession: T36472
A;Accession: Sceles A;Accession: A;Accession: A;Accession: Balance A;Accession: A;Accession: Balance A;Accession: Balance A;Accession: Balance A;Accession: Balance A;Accession: Balance B;Accession: Balance B;Accession: B;Accession:
RiOverbeeke, N.; Fellinger, A.J.; Toonen, M.Y.; van Wassenaar, D.; Verrips, C.T. Plant Mol. Biol. 13, 541-550, 1989
A;Title: Cloning and nucleotide sequence of the alpha-galactosidase cDNA from Cyamopsis A;Reference number: S07472; MUID:91370836; PMID:2577496
A;Refecession: S07472
A;Molecule type: mRNA
A;Residues: 1-411 <0VB>
A;Cross-references: UNIPROT:P14749; UNIPARC:UPI00001256A9; EMBL:X14619; NID:918291; PIDN A;Note: the authors translated the codon ATT for residue 20 as Asn, TAT for residue 140 C;Superfamily: alpha-galactosidase
C;Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 LGIYADVGNKTCA--GFPGSFGYYDIDAQTFADWGVDLLKFDGCYCDSLENLADGYKHMS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159 EEQDAKTFASWGVDYLKYDNC----ENLGISVKERYPPMGKALLSSGRPIFFSMCE--- 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YDIDAQTFADWGVDLLKFDGCYCDSLENLA----DGYKHMSLALNRTGRSIVYS-CEWPL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 -- WGWEDPQIW-AKSIGNSWRTTGDIEDNWNSMTSIADSNDKWASY-----AGPGGW 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NDPDMLVIGNFGLSWNQQVTQMALWAIMAAPLFMSNDLRHISPQAKALLQDKDVIAINQD 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCALALRFLALVSWDIPGARALDNGLARTPTMGWLHWERFMCNLDCQEEPDSCISEKLFM 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 GLAVSAQAVPAAAPDPAPASSGHEQLALTPPMGFNNWN----STHCRDE----FNESMVK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 DNGLARTPIMGWLHWERFMCNLDCQEEPDSCISEKLFMEMABLMVSEGWKDAGYEYLCID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 YMWPFQKPNYTEIRQYCNHWRNFADIDDSWKSIKSILD----WTSFNQERIVDVAGPGGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39;
                                                                                                                                                                                                                                                                                                                                                                                                    Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 680;
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Best Local Similarity 38.2%; Pred. No. 8.9e-50;
Matches 161; Conservative 67; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 29.5%; Score 681.5; DB 2; Best Local Similarity 42.2%; Pred. No. 1.5e-50; Matches 141; Conservative 52; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323 PLGKQGYQLRQGDNFEVWERPLSGLAWAVAMINR 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              320 KLGVQGKKVKSTNDLEVWAGPLSDNKVAVILWNR 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>..</u>
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A;Residues: 1-469 <TUR>
A;Residues: 1-469 <TUR>
A;Cross-references: UNIPROT:Q99172; UNIPARC:UPI0000696F1; EMBL;L24957; NID:g538518; PI
C;Genetics:
A;Gene: MEL
C;Superfemily: alpha-galactosidase
C;Superfemily: alpha-galactosidase; hydrolase
C;Reywords: glycoprotein; glycosidase; hydrolase
P;1-17/Domain: signal sequence #status predicted <NAT>
P;18-469/Product: alpha-galactosidase MEL #status predicted <NAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 SAGEYTCAGYAGSLGYEDMDAATFASWDVDYLKYDNCYNKGEFGTPEISYKRYKAMSDAL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LWAIMAAPLFMSNDLRHISPQAKALLQDKDVIAINQDPLGKQG----YQLRQGDNF--- 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|||::||: |: |: ::: : ||||||| ||
281 MWAIVKSPLIIGADIDDLKDSSLSVYSNPAVIAINQDVLGTPATRIWKYHVSDKDQYGEG 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 MVSEGWKDAGYEYLCIDDCWMAPQRDSEGRLQADPQRFPHGIRQLANYVHSKGLKLGIYA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 DVGNKTCAGFPGSFGYYDIDAQTFADWGVDLLKFDGCY----CDSLENLADGYKHMSLAL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 NKTGRPIFYSLCNWGQDLTFYWG-----SAISNSWRMSGDVYPQFDRPDSRCPCSG 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 FLALV--SWDIPGARALDNGLARTPTMGWLHWERFMCNLDCQEEPDSCISEKLFMEMAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FFALFFSSTDVLAASPSYNGLGLTPQMGWDNWNSFGCS------VKBELLLGTAEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---DDSWK----SIKSILDWTSFNQERIVDVAGPGGWNDPDMLVIGNFGLSWNQQVTQMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 DEYDCSYPGFHCSIMNILNKAAPMGQN----AAPGGWNDLDMLEVGVGNMSDSEEVAHFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 NRTGRSIVYS-CEWP---LYMWPFQKPNYTEIRQYCNHWRNFADI-------
                                                                                                                                                                                                                                                                                                                                24.1%; Score 557; DB 2; Length 469; 35.3%; Pred. No. 8.7e-40; cive 52; Mismatches 128; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       completed: December 24, 2005, 09:12:46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341 EIQLWSGPLDNGDHVVALLN 360
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 35.3%
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Job time : 42 secs
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                                                                                                                                                                                                Allegrante names: melibiase
C;Species: Mortierella vinacea
C;Species: Biochem: Jacchem. 61, 592-598, 1997
A;Title: Purification, characterization, and cDNA cloning of a novel alpha-galactosidase
A;Reference number: JG5558; MUID:97290877; PMID:9145516
A;Reference number: JG5558; MUID:97290877; PMID:9145516
A;Residues: 1-396 <SHI>
A;Residues: 1-396 <SHI>
A;Residues: 1-396 <SHI>
A;Residues: 1-396 <SHI>
A;Accession: PC4479
A;Accession: PC4479
A;Accession: PC4479
A;Accession: PC4479
A;Molecule type: protein
A;M
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NyAlernate names: MEL protein
Sipecies : Zygosaccharomyces cidri
C;becies: Zygosaccharomyces cidri
C;bate: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: S45453
R;Turakannen, H; Hankaanpaeae, M.; Korhola, M.; Aho, S.
Yeast 10, 73-745, 1994
A;Title: Characterization of MEL genes in the genus Zygosaccharomyces.
A;Accession: S45453
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -CEWPL-YMWPFQKPNYTEIRQYCNHWRNFADIDDSWKSIKSILDWTSFNQERIVDVAGP 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 GGWNDPDMLVIG-NFGLSWNQQVTQMALWAIMAAPLFMSNDLRHISPQAKALLQDKDVIA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 YYDIDAOTFADWGVDLLKFDGCYCDSLENL-----ADGYKHMSLALNRTGRSIVYS 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 YEAIDAQAFSDWGVDYLKYDNC----NNLGLACNATISSKRYKRMGDALKNVSRPIFFS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 IDPSLAKTPOMGWNSWNKYQCN------VNETVIINTANAMVSSGLKDLGYHYINI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 25.8%; Score 598; DB 2; Length 396;
Best Local Similarity 37.4%; Pred. No. 2.1e-43;
Matches 126; Conservative 57; Mismatches 116; Indels 38; Gaps
                                                                                                                                                                                         pha-galactosidase (EC 3.2.1.22) II precursor - Mortierella vinacea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                319 INQDPLGKQGYQLRQGDNFEVWERPLSGLAWAVAMIN 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 ISQDSLGASVQQRSMKGNTQLFAGFLSKNGYVSLFLN 333
   YIELFSGRLSNNDWVVAVLN 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92
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Gaps

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- nucleic search, using sw model OM nucleic

Run on:

December 26, 2005, 04:08:03; Search time 6366 Seconds (without alignments) 11304.400 Million cell updates/sec

US-10-602-219-11 1266 1 atgcagctgaggaacccaga......agctagaaaacacaatgtaa 1266 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

5883141 seqs, 28421725653 residues : <u>.</u> Searched:

11766282 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

GenEmbl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ΩI	AR653696	AR654964	AR653697	AR654965	AR653694	AR654962	AR653692	AR654960	AR653695	AR654963	AR653693	AR654961	CS135670	BT006864	AY889631	AY889632	AY892090	BT007835
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	* Query Match Length DB	1266	1266	1284	1284	1278	1278	1290	1290	1296	1296	1308	1308	1290	1290	1290	1290	1290	1290
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Garger,S.J., Turpen,T.H. and Kumagai,M.H.
Production of lysosomal enzymes in plants by transient expression
Patent: US 687696-A 7 03-MAY-2005;
Large Scale Biology Corporation; Vacaville, CA
Location/Qualifiers
                                                                         AGTATCTTGGACTGGACATCTTTTAACCAGGAGAGAATTGTTGATGTTGCTGGACCAGGG
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Garger, S.J., Turpen, T.H. and Kumagai, M.H.

Production of 19sosomal enzymes in plants by the charles i US 6890748-A 13 10-MAY-2005;

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Decide	REFERENCE 1 (bases 1 to 1290) AUTHORS Garget, S.J., Turpen, T.H. and Kumagai, M.H. TITLE Production of lysosomal enzymes in plants by transient expression JOURNAL Large Scale Biology Corporation; Vacaville, CA Location/Qualifiers 1. 1290 Location/Qualifiers 1. 1290 Authors Location/Qualifiers 1. 1290 Authors Authors Location/Qualifiers 1. 1290 Authors Authors

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Patent: US 6887696-A 5 03-MAY-2005;
Large Scale Biology Corporation; Vacaville, C
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61 CAGTHATTCOANTCACTCCCCAMATTTTCCTCCAMATTTTCCTCCAMAAGTNTAAG 720 62 [Patent: US 6890748-A \$ 10-MAY-2005; Large Scale Biology Corporation; Vacaville, CA Location/Qualifiers 1. :1308 / Organism="unknown" /mol_type="genomic DNA" /mol_type="genom

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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Homo sapiens galactosidase, alpha mRNA, complete cds.
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Crystal structure of human a-galactosidase
Crystal structure of human a-galactosidase
Satent: WO 2005069192-A 1 28-UUL-2005;
Transkaryotic Therapies, Inc. (US); Selden, Richard F. (US);
Garboczi, David N. (US); Treco, Douglas A. (US); NIH/NIAID (US);
Garman, Scott C. (US); Borowski, Marianne (US); Kinoshita, Carol M. (US)
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Sequence 1 from Patent WO2005069192.
CS135670 GI:72056330
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1. .1290
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Pred. No. 0;
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Homo sapiens (human)
Homo sapiens
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AY889631 1290 bp mRNA linear SYN 29-MAR-2005 Synthetic construct Homo sapiens clone FLH025769.01X galactosidase alpha (GLA) mRNA, complete cds.
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S Kalnin, N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Phelan,M. and Farmer,J. Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Phelan,M. and Farmer,J. Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Phelan,M. and Farmer,J. Busciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA

This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been the Sall and HindIII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after Sall site and before HindIII site to maintain reading frame.

Clone distribution: http://bioinfo.clontech.com/orfclones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="molrnpelhiggalarize"/transperdingarizethgm
LHWERFMCNIDCQEEPDSCISEKIFMEMAELMVSEGWKDAGYEYLCIDDCWMAPQRDS
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  Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M. and Farmer, A.
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/mol_type="mRNA"
/do Xref="naxon:9606"
/do Arref="axon:9606"
/clone="GHO0112X1.0"
/clone=lib="BD Creator(TM) CDS Library derived from MGC
collection"
/lab_host="DH5alpha T1 resistant"
/note="Vector: pDNR-Dual"
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                                                                              Cloning of human full-length CDSs in BD Creator (TM) System
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protein_id="AAP35510.1"
db_xref="G1:30582567"
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                                                                                                                     GATTCAGAAGGCAGACTTCAGGCAGACCCTCAGCGCTTTCCTCATGGGATTCGCCAGCTA
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                                                      TGGAAGGATGCAGGTTATGAGTACCTCTGCATTGATGACTGTTGGATGGCTCCCCAAAGA
                                                                                                                                                                                       GCTAATTATGTTCACAGCAAAGGACTGAAGCTAGGGATTTATGCAGATGTTGGAAATAAA
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                                                                                                                                                                                                                                                                                    Direct Submission

L Submitted (04-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA

This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics.

This ORF clone has been cloned with normalized stop-codon. The CDS has been directionally cloned using BD In-Rusion(TM) cloning system between the Sall and HindIII sites of the pDNR-Dual vector.

Additional sequences in the clone: 'ACC' after Sall site and before 'ATG' to provide Kozak consensus sequence. Each clone is clonally isolated and full-length sequence-verified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DWGVDLLKFDGCYCDSLENLADGYKHWSLALNRTGRSIVYSCEWPLYMPFQKDNYTE
IROYCNHWRNFADIDDSWKSIKSILDWTSFNQERIVUVAGPGGWNDPDMLVIGNFGLS
WNQOVTQMALWAIMAAPLEMSUDLHISPQAKALLQDKDVIAINQDPLGKQGYQLRQG
DNPEVWBRPLSGLADANVAMIRRQEIGGPRSYTIAVASLGKGVACNPACFITQLLPVKR
KLGFYEWTSRLRSHINPTGTVLLQLENTWQMSLKDLL"
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               AY889631.1 GI:60655716
Human ORF Project.
synthetic construct
synthetic construct
other sequences; artificial sequences.

other sequences; artificial sequences.

i (bases I to 1290)
Hines, L., Rolfs, A., Yepson, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J. and LaBaer, J.

Cloning of human full-length CDS in Creator (TM) recombinational vector system
Unpublished
                                                                                                                                                                                                                        2 (bases 1 to 1290)
hines, L., Rolfs, Jepson, D., Moreira, D., Raphael, J., Kelley, F.,
Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,
Williamson, J. and LaBaer, J.
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/mol_type="mRNA"
/Mol_xref="texxon:32630"
/Lb_xref="texxon:32630"
/clone="FLH4025769.01X"
/lab_host="Escherichia coli DH5alpha Tl resistant"
/note="derived from MGC template"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.7%; Score 1261.8; DB 11; Length 1290; 99.8%; Pred. No. 0;
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Matches 1263; Conservative
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Search completed: December 26, 2005, 07:09:28 Job time : 6371 secs

December 26, 2005, 01:02:18; Search time 771 Seconds (without alignments) 10943.581 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. - nucleic search, using sw model OM nucleic Run on:

US-10-602-219-11 1266 1 atgcagctgaggaacccaga......agctagaaaacacaatgtaa 1266 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 **.**.. Scoring table:

4996997 segs, 3332346308 residues

Searched:

9993994 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn2003cs:*
geneseqn2003ds:*
geneseqn2004as:*
geneseqn2004bs:* N. Geneseq 21:*
1: geneseqn1980s:*
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9: geneseqn2003as:* 10: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Query Match Length DB	DB	ti.	Description
٦	1266	100.0	1266	φ	AAD45223	Aad45223 Human rGA
7	1266	100.0	1266	10	ADD84750	Add84750 Human alp
e	1266	100.0	1266	12	ADJ88276	Adj88276 Human WT
4	1266	100.0	1266	12	ADM48680	Adm48680 Human wil
S	1266	100.0	1266	13	ADU66915	Adu66915 Human alp
9	1266	100.0	1266	14	AEA27444	Aea27444 Human alp
7	1264	8.66	1284	9	AAD45224	Aad45224 Human rGA
ω	1264	8.66	1284	10	ADD84752	Add84752 Human alp
თ	1264	8.66	1284	12	ADJ88278	Adj88278 Human WT
10	1264	99.8	1284	12	ADM48682	Adm48682 Human wil
11	1264	99.8	1284	13	ADU66917	Adu66917 Human alp
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17	1263.4	99.8	1278	13	ADU66911	Adu66911 Human alp
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1290 10 ADD84742 1290 12 ADD88268 1290 13 ADM48672 1296 14 AEAA7436 1296 6 AAD45222 1296 12 ADD884748 1296 12 ADD88774 1296 13 ADD66913 1296 13 ADM48678 1308 10 ADD84744 1308 11 ADD84744 1308 12 ADM48674 1308 12 ADM48674 1308 13 ADM48674 1308 13 ADM48674 1309 13 ADM48739 1290 13 ADM74415 1290 13 ADM74415 1391 10 ADH54464 1343 3 AAA75434 1343 3 AAA75434	Add84742 Human alp Adj88268 Human WT Adm48672 Human wil Acac66907 Human alp Aca27436 Human alp Aca27436 Human alp Aca45222 Human alp Adj88274 Human WT Adm48678 Human wil Aca27442 Human alp Aca27442 Human alp Aca27442 Human alp Aca27444 Human alp Aca27444 Human alp Aca45220 Human alp Aca48678 Human alp Aca6890 Human wil Ach66909 Human wil Ach66909 Human wil	Aduray 1.9 human alp Aduray 1.5 human alp Ab43187 human alp Ab43187 human alp Acf80581 human alp Adh54464 human alp Aaa731801 hucleotid Aaa75434 Nucleotid Aaa70685 human alp
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ALIGNMENTS

Human; alpha-galactosidase; lysosomal enzyme; lysosomal storage disease; therapeutic; rGAL-8; gene; ds. Location/Qualifiers 1. 1266 /*taga a /product= "Human rGAL-8 protein" AAD45223 standard; DNA; 1266 BP (first entry) Human rGAL-8 DNA. US2002088024-A1. 27-DEC-2002 Homo sapiens 04-JUL-2002. AAD45223; Key RESULT 1 AAD4 5223

13-NOV-2001; 2001US-00993059.

26-JUL-2000; 2000US-00626127.

(GARG/) GARGER S J. (TURP/) TURPEN T H. (KUMA/) KUMAGAI M H.

Kumagai MH; Garger SJ, Turpen TH,

WPI; 2002-681656/73. P-PSDB; AAE28210.

Novel human alpha-galactosidase polypeptide useful for treating lysosomal storage diseases.

Claim 1, Page 42-44; 88pp; English.

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1201 TCAAGGTTAAGAAGTCACATAAATCCCACAGGCACTGTTTTGCTTCAGCTAGAAAACACA 1260
                                                                                                                                            CAGGACCCCTTGGGCAAGCAAGGGTACCAGCTTAGACAGGGAGACAACTTTGAAGTGTGG
                  GTAACTCAGATGGCCCTCTGGGCTATCATGGCTGCTCCTTTATTCATGTCTAATGACCTC
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1. .1266
/*tag= a
/product= "Human rGAL-8"
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13-NOV-2001; 2001US-00993059.
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(TURP/) TURPEN T H.
(KUMA/) KUMAGAI M H.
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The invention relates to human alpha-galactosidase truncated at the carboxy terminus and the production of enzymatically active recombinant human and animal lysosomal enzymes. The invention is useful for producing lysosomal enzymes for treating lysosomal storage diseases, producing altered or mutated proteins, enzymatically active or otherwise, to serve as precursors or substrates for further in vivo or in vitro processing to a specialised industrial form for research or therapeutic uses, to produce more effective therapeutic enzyme, for producing antibodies against lysosomal enzymes for medical diagnostic use, and in any sequence is human rGAL-8 DNA
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Fabry's disease; Gaucher's disease; human; gene; ds.
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1. https a
/product= "Human WT rGAL-8 protein"
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08-JUN-1989;
22-OCT-1990;
16-JAN-1991;
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31-JUL-1992;
30-DEC-1992;
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  enzymes in a plant expression system that can be used in enzyme
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                                                                                                                The invention relates to human alpha-galactosidase derivatives and the nucleic acids encoding them. The polypeptides are used in a method for producing active recombinant human and animal lysosomal enzymes in a plant expression system. The enzymes can be used in enzyme replacement therapy for the therapeutic treatment of human and animal lysosomal diseases. This sequence represents DNA encoding a human alpha-galactosidase derivative polypeptide of the invention.
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Best Local Similarity 100.
Matches 1266; Conservative
                              replacement therapy.
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lysosomal storage disease; Gaucher's disease; Niemann-Pick disease;
Pabry disease; Tay-Sachs disease; cardiovascular; nephrotrophic; human;
                                                                       601 TCCTGTGAGTGGCCTCTTTATATGTGGCCCTTTCAAAAGCCCAATTATACAGAAATCCGA
                                                                                                                                                                                                                                                                     GTAACTCAGATGGCCCTCTGGGCTATCATGGCTGCTCCTTTATTCATGTCTAATGACCTC
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                                                                                                                                 AGTATCTTGGACTGGACATCTTTTAACCAGGAGAATTGTTGATGTTGCTGGACCAGGG
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                                                                                                                                                                                             GGTTGGAATGACCCCAGATATGTTAGTGATTGGCAACTTTGGCCTCAGCTGGAATCAGCAA
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                                                                                                                                                                                                                                                     human and animal lysosomal Gaucher's diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 1266; DB 12; Length 1266;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1266; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                   U; 0 Other;
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                                                                                                                                                                                                                                                     New lysosomal enzymes, useful in treating h
storage diseases, e.g. Fabry's disease and
                                                                                                                                                                              Grill
                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 11; 71pp; English.
                                                                                                                                                                              RL,
29-DEC-1993; 93US-00176414.

19-JAN 1994; 94US-00184237.

14-OCT-1994; 94US-00324003.

21-MAY-1999; 99US-00316572.

26-JUL-2000; 2000US-00626127.

13-NOV-2001; 2001US-00993059.
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P-PSDB; ADJ88277.
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                GCTAATTATGTTCACAGCAAAGGACTGAAGCTAGGGATTTATGCAGATGTTGGAAATAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to novel galactosidase (Gal) proteins such as rGAL-12, rGAL-12R, r-GAL-25 or rGAL-25R. The methods and compositions of the present invention are useful for producing recombinant lysosomal enzymes for enzyme replacement therapy for treating human and animal lysosomal storage diseases sucher's adisease. Niemann-Pick disease, Rabry disease and Tay-Sachs disease. The present sequence is human wild type rGAL-8 DNA used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             New alpha-galactosidase polypeptides, useful in producing recombinant lysosomal enzymes for the treatment of lysosomal storage diseases, such as Gaucher's disease, Niemann-Pick disease, Fabry disease and Tay-Sachs
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                                                         88US-00160766.
88US-00160771.
89US-0031081.
90US-0060244.
92US-00923692.
92US-00937733.
93US-00184237.
94US-00184237.
94US-00184237.
94US-00324003.
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POGUE G P.
ERWIN R L.
GRILL L K.
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P-PSDB; ADM48681.
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Matches 1266; Conserv
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21-MAY-1999;
26-JUL-2000;
13-NOV-2001;
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31-JUL-1992;
30-DEC-1992;
29-DEC-1993;
19-JAN-1994;
                               23 - JUN - 2003;
                                                           26-FEB-1988;
26-FEB-1988;
17-FEB-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to the production of human and animal lysosomal enzymes in plants by a transient plant expression system. The invention relates to glucocerebrosidase (GCB, GCR) and alphagalactosidase enzymes having a post-translational modification provided by the plant expression system. The invention is useful in enzyme replacement therapy for treating lysosomal storage diseases such as Gaucher's disease, Niemann-Pick disease, Eabry's disease and Tay-Sachs disease, Hurler's syndrome and Hurler-Scheie syndrome. The invention is also useful in researches for developing new approaches to medical treatment of lysosomal storage diseases and in industrial processes involving enzymatic substrate hydrolysis. The present sequence is the
                                                                                                                                                                                                                                                                                                                                                                              for
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                                Lygosowal enzyme; glucocerebrosidase; GCB; GCR; alpha-galactosidase; enzyme replacement therapy; lysosomal storage disease; Gaucher's diseann-bick disease; Pabry's disease; Alsease; Hurler's syndrome; Hurler's syndrome; nephrotropic; human; gene;
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                                                                                                                                                   "Human alpha-galactosidase protein"
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            alpha-galactosidase protein encoding DNA #5
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                                                                                                                Location/Qualifiers
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/product= "Human alph
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13-NOV-2001; 2001US-00993059.
20-MAR-2002; 2002US-00103327.
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Best Local Similarity
Matches 1266; Conserv
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                                                                                                                                                            Gauchers disease; metabolic; neurological disease; niemann pick disease; genetic disorder; Fabry disease; metabolic disorder; tay sachs disease; antilipemic; cns-gen.; lysosome storage disease; alpha-galactosidase; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to the production of human and animal lysosomal enzymes in plants by a transient plant expression system. The invention relates to glucocarebrosidase (GCB, GCR) and alpha-invention relates to glucocarebrosidase (GCB, GCR) and alpha-galactosidase (Gal) enzymes having a post-translational modification provided by the plant expression system. The invention is useful in enzyme replacement therapy for treating lysosomal storage diseases such as Gaucher's disease, Niemann-Pick disease, Fabry's disease, Tay-Sachs disease, Hurler's syndrome and Hurler-Scheie syndrome. The invention is also useful in researches for developing new approaches to medical treatment of lysosomal storage diseases and in industrial processes involving enzymatic substrate hydrolysis. The present sequence is the
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/product= "Human alpha-galactosidase protein"
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                                 AEA27444 standard; DNA; 1266 BP
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13-NOV-2001; 2001US-00993059.
20-MAR-2002; 2002US-00103327.
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Best Local Similarity 100.0%;
Matches 1266; Conservative 0
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invention is useful in gene therapy. The polynucleotides and polypeptides are useful in treating human and animal lysosomal storage diseases, e.g. Fabry's disease and Gaucher's diseases. The present sequence is human GAL DNA.
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                                                                 1201 TCAAGGTTAAGAAGTCACATAAATCCCACAGGCACTGTTTTGCTTCAGCTAGAAAACACA 1260
            The invention relates to nucleotide encoding galactosidase (GAL). The
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                                                                                                                                                                                                                                                                                                       disease;
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1..1284
/*tag= a
/product= "Human WT rGAL-8R protein"
                                                                                                                                                                                                                                                                                                    Galactosidase; GAL; gene therapy; lysosomal storage Fabry's disease; Gaucher's disease; human; gene; ds.
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26-FEB-1988; 88US-00160771.
17-FEB-1989; 89US-003108279.
17-FEB-1989; 89US-003108279.
18-JUL-1989; 89US-00347637.
22-OCT-1990; 90US-0060244.
16-JAN-1991; 91US-0063143.
11-JUL-1991; 91US-00737899.
01-AUG-1991; 91US-00737899.
01-AUG-1992; 92US-00923692.
01-AUG-1992; 92US-00937892.
01-AUG-1992; 93US-00116414.
01-AUG-1994; 94US-00184237.
01-AUG-2000; 2000US-00626127.
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P-PSDB; ADJ88279.
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POGUE G P.
ERWIN R L.
GRILL L K.
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The present invention relates to novel galactosidase (Gal) proteins such as rGAL-12, rGAL-12R, r-GAL-25 or rGAL-25R. The methods and compositions of the present invention are useful for producing recombinant lysosomal enzymes for enzyme replacement therapy for treating human and animal lysosomal storage diseases such as Gaucher's disease, Niemann-Pick disease, Fabry disease and Tay-Sachs disease. The present sequence is human wild type rGAL-8R DNA. This sequence comprises a human rGAL-8 DNA and Ex retention signal DNA. This sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ACCATGGGCTGGCTGCACTGGGAGCGCTTCATGTGCAACCTTGACTGCCAGGAAGAGCCA 180
                                                                                                                  New alpha-galactosidase polypeptides, useful in producing recombinant lysosomal enzymes for the treatment of lysosomal storage diseases, such as Gaucher's disease, Niemann-Pick disease, Fabry disease and Tay-Sachs
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Matches 1264; Conservative
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lysosomal storage disease; Gaucher's disease; Niemann-Pick disease;
Fabry disease; Tay-Sachs disease; cardiovascular; nephrotrophic; human;
                                     CGACACATCAGCCCTCAAGCCCAAAGCTCTCCTTCAGGATAAGGACGTAATTGCCATCAAT
                                                                                                                                                                                              GGACCTCGCTCTTATACCATCGCAGTTGCTTCCCTGGGTAAAGGAGTGGCCTGTAATCCT
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92US-00923692.

92US-0093733.

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99US-00186572.
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POGUE G P.
ERWIN R L.
GRILL L K.
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26-JUL-2000;
13-NOV-2001;
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17-FEB-1989;
22-OCT-1990;
31-JUL-1992;
30-DEC-1992;
29-DEC-1993;
14-OCT-1994;
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                                                                                                                                                                 A pharmaceutical composition comprising a lysosomal enzyme, useful enzyme replacement therapy for the treatment of lysosomal storage diseases, such as Fabry's disease.
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100.0%; Pred. No. 0;
ive 0; Mismatches
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                                                           (LARG-) LARGE SCALE BIOLOGY CORP.
26-JUL-2000; 2000US-00626127.
13-NOV-2001; 2001US-00993059.
20-MAR-2002; 2002US-00103327.
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Matches 1264; Conservative
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                   CAGTACTGCAATCACTGGCGAAATTTTGCTGACATTGATGATTCCTGGAAAAGTATAAAG
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13-NOV-2001; 2001US-00993059.
20-MAR-2002; 2002US-00103327.
                                                                               08-NOV-2004; 2004US-00984389
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Matches 1264; Conservative
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The invention relates to human alpha-galactosidase truncated at the carboxy terminus and the production of enzymatically active recombinant human and animal lysosomal enzymes. The invention is useful for producing lysosomal enzymes for treating lysosomal storage diseases, producing altered or mutated proteins, enzymatically active or otherwise, to serve as precursors or substrates for further in vivo or in vitro processing to a specialised industrial form for research or therapeutic uses, to produce more effective therapeutic enzyme, for producing antibodies against lysosomal enzymes for medical diagnostic use, and in any commercial process that involves substrate hydrolysis. The present
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                                                                                                                                                                                                                                                       Kumagai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence is human rGAL-4 DNA
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Matches 1264; Conservative
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ds; lysosomal
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Human; alpha-galactosidase; rGAL-4; gene; ds;
enzyme replacement therapy; lysosomal disease
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Pred. No. 0;
0; Mismatches
                                                                          "Human rGAL-4"
                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 7; 77pp; English.
                                              Location/Qualifiers
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                                                                                                                                                                                                                      Kumagai
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13-NOV-2001; 2001US-00993059
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/product=
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/*tag= a
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P-PSDB; ADD84747.
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TURPEN T H.
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GCTAATTATGTTCACAGCAAAGGACTGAAGCTAGGGATTTATGCAGATGTTGGAAATAAA
                             ACCTGCGCAGGCTTCCCTGGGAGTTTTGGATACTACGACATTGATGCCCAGACCTTTGCT
                                                        GACTGGGGAGTAGATCTGCTAAAATTTGATGGTTGTTACTGTGACAGTTTGGAAAATTTG
                                                                   GACTGGGGGAGTAGATCTGCTAAAATTTGATGGTTGTTACTGTGACAGTTTGGAAAATTTG
                                                                                             GCAGATGGTTATAAGCACATGTCCTTGGCCCTGAATAGGACTGGCAGAAGCATTGTGTAC
                                                                                                        GCAGATGCTTATAAGCACATGTCCTTGGCCCTGAATAGGACTGGCAGAGCATTGTGTAC
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New polynucleotide for producing active recombinant human and animal lysosomal enzymes in a plant expression system that can be used in enzyme 241 regaacearecacerrareacracerecearreareacrerresarescrececeaasa 300 The invention relates to human alpha-galactosidase derivatives and the nucleic acids encoding them. The polypeptides are used in a method for producing active recombinant human and animal lysosomal enzymes in a plant expression system. The enzymes can be used in enzyme replacement therapy for the therapeutic treatment of human and animal lysosomal diseases. This sequence represents DNA encoding a human alpha-galactosidase derivative polypeptide of the invention. CTCGTTTCCTGGGACATCCCTGGGGCTAGAGCACTGGACAATGGATTGGCAAGGACGCCT 1 ATGCAGCTGAGGAACCCAGAACTACATCTGGGCTGCGCGCTTGCGCTTCGCTTCCTGGCC CTCGTTTCCTGGGACATCCCTGGGGCTAGAGCACTGGACAATGGATTGGCAAGGACGCCT 121 ACCATGGGCTGCACTGGGAGCGCTTCATGTGCAACCTTGACTGCCAGGAAGAGCCA GATTCAGAAGGCAGACTTCAGGCAGACCCTCAGGCGCTTTCCTCATGGGATTCGCCAGCTA 1 ATGCAGCTGAGGAACCCAGAACTACATCTGGGCTGCGCGCTTGCGCTTCGCTTCCTGGCC GATTCCTGCATCAGTGAGAAGCTCTTCATGGAGATGGCAGAGCTCATGGTCTCAGAAGGC TGGAAGGATGCAGGTTATGAGTACCTCTGCATTGATGACTGGTTGGATGGCTCCCCAAAGA GATICAGAAGGCAGACTICAGGCAGACCCICAGGCGCTITCCTCATGGGATICGCCAGCTA Gaps Length 1278 ö Sequence 1278 BP; 325 A; 293 C; 333 G; 327 T; 0 U; 0 Other; 1; Indels

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The invention relates to nucleotide encoding galactosidase (GAL). The invention is useful in gene therapy. The polynucleotides and polypeptides are useful in treating human and animal lysosomal storage diseases, e.g. Fabry's disease and Gaucher's diseases. The present sequence is human GAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCGTTTCCTGGGACATCCCTGGGGCTAGAGCACTGGACAATGGATTGGCAAGGACGCCT 120
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                Galactosidase, GAL, gene therapy, lysosomal storage Fabry's disease, Gaucher's disease, human, gene, ds.
                                                                              Location/Qualifiers
1. .1278
/*tag= a
/product= "Human WT rGAL-4 protein"
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                                                                                                                                                    /note= "No start codon"
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26-FEB-1988; 8BUS-00160771.

17-FEB-1989; 8BUS-00131281.

05-MAY-1989; 89US-00313138.

02-CUN-1989; 89US-00347537.

02-CUN-1989; 89US-003471318.

26-CUN-1991; 91US-00641617.

26-CUN-1991; 91US-00737899.

01-AUG-1991; 91US-00737899.

01-AUG-1991; 91US-00737899.

01-AUG-1992; 92US-0099733.

01-DEC-1992; 92US-0099733.

01-DEC-1994; 94US-0016414.

19-JAN-1994; 94US-0016414.

19-JAN-1994; 94US-0016417.

11-MAY-1994; 99US-0016572.

26-UUL-2000; 2000US-00316572.

26-UUL-2000; 2000US-00316572.
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Best Local Similarity 99.9%;
Matches 1264; Conservative
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P-PSDB; ADJ88273.
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Gaps

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Length 1278;

ACCATGGGCTGGCTGCGCTGGGGGCTTCATGTGCAACCTTGACTGCCAGGAAGAGCCA 180	TTCCTGCATCAGTGAGAGCTCTTCATGGAGATGGCAGAGCTCATGGTCTCAGAAGGC 240	TGGAAGGATGCAGGTTATGAGTACCTCTGCATTGACTGTTGGATGGCTCCCCAAAGA 300	GATTCAGAAGGAGACTTCAGGCAGACCTCAGCGCTTTCCTCATGGGATTCGCCAGCTA 360	CTAATTATGTTCACAGCAAAGGACTGAAGCTAGGGATTTATGCACATGTTGGAAATAAA 420 	ACCIGCGCAGGCITCCCTGGGAGTITTGGATACTACGACATTGATGCCCAGACCTTTGCT 480	GACTIGGGGAGTAGATCTGGTAAATTTGATGGTTGTTACTGTGACAGTTTGGAAATTTG 540 	CAGATGGTTATAAGCACATGTCCTTGGCCCTGAATAGGACTGGCAGAAGCATTGTGTAC 600	CCTGTGAGTGGCCTCTTTATATGTGGCCCTTTCAAAAGCCCAATTATACAGAAATCCGA 660	CAGTACTGCAATCACTGGCGAAATTTTGCTGACATTGATGATTCCTGGAAAAGTATAAAG 720 	AGTATCTTGGACTGGACATCTTTTAACCAGGAGAATTGTTGATGCTGGTGGACCAGGG 780	GGTTGGAATGACCCAGATATGTTAGTGATTGGCAACTTTGGCCTCAGCTGGAATCAGCAA 840 	GTAACTCAGATGGCCCTCTGGGCTATCATGGCTGCTTATTCATGTCTAATGACCTC 900	CGACACATCAGCCCTCAAGCCAAAGCTCTCCTTCAGGATAAGGACGTAATTGCCATCAAT 960 	CAGGACCCCTTGGGCAAGGGTACCAGCTTAGACAGGGACAACTTTGAAGTGTGG 1020 	GAACGACCTCTCTCAGGCTTAGCCTGGGGCTGTAGCTATGATAAACCGGCAGGAGATTGGT 1080 	GGACCTCGCTCTTATACCATCGCAGTTGCTTCCCTGGGTAAAGAGTGGCCTGTAATCCT 1140 	GCCTGCTTCATCACACAGGTCCTCCCTGTGAAAAGGAAGCTAGGTTCTATGAATGGACT 1200 	TCAAGGTTAAGAAGTCACATAAATCCCACAGGCACTGTTTTGCTTCAGGTAGAAAACACA 1260
121 ACC 	181 GATTC 181 GATTC	241 TGC 241 TGC	301 GA7 301 GA7	361 GC 	421 ACC 421 ACC	481 GA(481 GA(541 GC 541 GC	601 TC 	661 CAC 	721 AG 721 AG	781 GG7 	841 GT2 841 GT2	901 CG/ 	961 CAC 	1021 GAJ 	1081 GG 	1141 GC 1141 GC	1201 TC

8 6 6 6

6 6 6 6 6 6

1201 TCAAGGTTAAGAAGTCACATAAATCCCACAGGCACTGTTTTGCTTCAGCTAGAAAACACA 1260 1261 ATGTA 1265 1261 ATGCA 1265 . ብ ሪ ብ

Search completed: December 26, 2005, 05:23:09 Job time : 775 secs

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December 26, 2005, 04:17:59; Search time 4817 Seconds (without alignments) 12296.543 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on:

US-10-602-219-11 1266 1 atgcagctgaggaacccaga......agctagaaaacacaatgtaa 1266 Title: Perfect score:

Sequence:

41078325 segs, 23393541228 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table: Searched:

Total number of hits satisfying chosen parameters:

82156650

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

1: 9b est1:*
2: 9b est2:*
3: 9b est3:*
5: 9b est5:*
6: 9b est5:*
7: 9b est6:*
8: 9b est7:*
9: 9b gss1:*
11: 9b gss2:* EST:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	CR605654 full-leng	CR607242 full-leng	CR617861 full-leng	AY408540 Homo sapi	AY408541 Pan trogl		BX354096 BX354096	AL552630 AL552630	BM564282 AGENCOURT	AL577581 AL577581	AK054547 Mus muscu	AK040081 Mus muscu	CO645672 ILLUMIGEN	CO645623 ILLUMIGEN	AL575861 AL575861	BQ062192 AGENCOURT	CO646251 ILLUMIGEN	CO645464 ILLUMIGEN	CT005156 CT005156	AY408542 Mus muscu	BQ956043 AGENCOURT	BQ934640 AGENCOURT
ID	CR605654	CR607242	CR617861	AY408540	AY408541	AL554978	BX354096	AL552630	BM564282	AL577581	AK054547	AK040081	C0645672	CO645623	AL575861	BQ062192	C0646251	C0645464	CT005156	AY408542	BQ956043	BQ934640
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% Query Match	99.7	99.4	98.6	92.4	90.8	76.5	73.2	72.9	72.3	72.3	71.1	71.1	70.3	69.8	9.69	69.1	68.7	68.1	67.6	65.5	64.3	63.8
Score	1261.8	1258.4	1248	1169.8	1149.4	968.6	926.8	922.8	915.8	915	8.668	899.8	890	883.2	880.8	874.6	870	862.4	856.4	828.6	814.2	807.8
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Gaps

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2; Indels

Query Match
99.7%; Score 1261.8;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1263; Conservative 0; Mismatches

DB 4; Length 1277;

BU540848 AGENCOURT	BU191867 AGENCOURT	BU154569 AGENCOURT	CA454083 AGENCOURT		_	_	_	-	CA487415 AGENCOURT	•		-	BE379425 601237275	BI224248 602940538	BQ225444 AGENCOURT		_	BG824387 602728627		-	CB529027 UI-H-FT2-	BI753664 603023559
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	62.8		61.8	60.7	60.5	29 765.2 60.4	60.1	59.8	59.4	59.1	59.0	59.0	59.0	58.7	58.6	39 741.4 58.6 10	58.5	58.2	57.6	57.5	56.4	55.2

ALIGNMENTS

RESULT 1	
CR605654	
LOCUS	CR605654 1277 bp mRNA linear HTC 21-JUL-2004
DEFINITION	full-length cDNA clone CSODB008YB11 of Neuroblastoma Cot
	10-normalized of Homo sapiens (human).
ACCESSION	
VERSION	CR605654.1 GI:50486461
KEYWORDS	HTC; CNSLT_CDNA.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini;
	Hominidae; Homo.
REFERENCE	1 (bases 1 to 1277)
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL :
	http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
	Faraday Avenue
REFERENCE	2 (bases 1 to 1277) .
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
	BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
	- Web : www.genoscope.cns.fr)
COMMENT	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
	end enriched, double-strand cDNA was digested with Not I and cloned
	into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
	was normalized. Library was constructed by Life Technologies, a
	division of Invitrogen.
FEATURES	Location/Qualifiers
source	11277
	/organism="Homo sapiens"
	/mol type="mRNA"
	/db xref="taxon:9606"
	/clone="CS0DB008YB11"
	/tissue_type="Neuroblastoma Cot 10-normalized"
	/plasmid="pCMVSPORT_6"
ORIGIN	

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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRV cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                   CR607242 1266 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CS0DI067YJ01 of Placenta Cot 25-normalized of Homos sapiens (human).
                                                                                                                                                                     CTCGTTTCCTGGGACATCCCTGGGGCTAGAGCACTGGACAATGGATTGGCAAGGACGCCT 120
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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127 ACCATGGGCTGGCTGCACGGAGCGCTTCATGTGCAACCTTGACTGCCAGGAAGAGCCA
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GGACCTCGCTCTTATACCATCGCAGTTGCTTCCCTGGGTAAAGAGAGTGGCCTGTAAATCCT
                                                             GCCTGCTTCATCACACACACCTCCTGTGAAAAGGAAGCTAGGGTTCTATGAATGGACT
                                                                                    GCCTGCTTCATCACACAGAGCTCCTCTGTGAAAAGGAAGCTAGGGTTCTATGAATGGACT
                                                                                                                                             TCAAGGTTAAGAAGTCACATAAATCCCACAGGCACTGTTTTGCTTCAGCTAGAAAACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1067YJ01"
/tissue_type="Placenta_Cot_25-normalized"
/plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hominidae, Homo.

1 (bases 1 to 1266)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished
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99.9%; Pred. No. 0;
:ive 0; Mismatches
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HTC; CNSLT cDNA.
Homo sapiens (human)
Homo sapiens
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2 (bases 1 to 1266)
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Best Local Similarity 99.9
Matches 1259; Conservative
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KEYWORDS
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DEFINITION
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TITLE
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                                                                                    CTCGTTTCCTGGGACATCCCTGGGGCTAGAGCACTGGACAATGGATTGGCAAGGACGCCT
                                                                                                              CTCGTTTCCTGGGACATCCCTGGGGCTAGAGCACTGGACAATGGATTGCCAAGGACGCCT
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr | 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                CR617861 1253 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CS0DK009YE12 of HeLa cells Cot 25-normalized of Homo sapiens (human).
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                           Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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1 (bases 1 to 1253)
Li W B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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98.6%; Score 1248; C
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches
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/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="CSODKOO9YE12"
/tissue_type="HeLa cells Cc
/plasmid="pcMVSPORT_6"
                                                                                                   CR617861.1 GI:50498668
HTC; CNSLT cDNA.
Homo sapiens (human)
Homo sapiens
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                                                                      TGGAAGGATGCAGGTTATGAGTACCTCTGCATTGATGACTGTTGGATGGCTCCCCAAAGA
                                                                                          247 TGGAAGGATGCAGGTTATGAGTACCTCTGCATTGATGACTGTTGGATGGCTCCCCAAAGA
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241 TGGAAGGATGCAGGTTATGAGTACCTCTGCATTGATGACTGTTGGATGGCTCCCCAAAGA 300
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        Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
1. 1290
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                                                                                                                                                                                                                 DB 10;
                                                                                            /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
                                                                                                                                                                                                              Score 1149.4;
Pred. No. 0;
0; Mismatches
                                                                                                                                                          /gene="GLA"
/locus_tag="HCM3258"
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Best Local Similarity 91.1%;
Matches 1153; Conservative C
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Pan troglodytes GLA gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Mominidae; Pan.
1 (Dases 1 to 1290)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Ford, M.A., Tanembaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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                             CAGTACTGCAATCACTGGCGAAATTTTGCTGACATTGATGATTCCTGGAAAAGTATAAAG
                                                                                                                               GGTTGGAATGACCCAGATATGTTAGTGATTGGCAACTTTGGCCTCAGCTGGAATCAGCAA
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CCGACACATCAGCCCTCAAGCCAAAGCTCTCCTTCAGGATAAGGACGTAATTGCCATCAA 959
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED" /note="lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR vites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                          Score 968.6; DB 1;
Pred. No. 8e-279;
); Mismatches 8;
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Matches 1012; Conservative
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Hominidae; Homo.

Li (bases 1 to 1086)

Li,W.B., Gruber, C., Jessee, J. and Polayes, D.

Pull-length cDNA libraries and normalization

Don Feb 15, 2001 this sequence version replaced gi:31276787.

Contact: Genscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: sequengeonoscope.cns.fr, Web: www.genscope.cns.fr

Ist strand cDNA was primed with a Not1-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the powV890PR v vector. Library

was normalized. Library was constructed by Life Technologies, a
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   GGTTGGAATGACCCAGATATGTTAGTGATTGGCAACTTTGGCCTCAGCTGGAATCAGCAA
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/mol_type="mRNA"
/db xref="taxon;9606"
/clone="KSODKO09YE12"
/cell_type="HEIA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
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Homo sapiens
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 TCAGTGAGAAGCTCTTCATGGAGATGGCAGAGCTCATGGTCTCAGAAGGCTGGAAGGATG 267
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 999)

11. (Bases 1 to 999)

12. (Bases 1 to 999)

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31274445.
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Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and Ecok V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
                                                        BX354096

1014 bp mRNA linear EST 23-APR-2004
BX354096 Homo sapiens NEUROBLASTOWA COT 25-NORWALIZED Homo sapiens
cDNA clone CSODC014YH04 5-PRIME, mRNA sequence.
BX354096.2 GI:46550107
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/tissue type="NEUROBLASTOMA COT 25-NORMALIZED"
/tissue type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone lib="Homo sapiens NEUROBLASTOWA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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CCGACACATCAGCCCTCAAGCCTAAGCTCTTCAGGATAAGGACGTWATTGCCATCAA 964
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                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euterchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1014)

1 (bases 1 to 2014)

1 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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                                     TCAGGACCCCTTGGGCAAGCAAGGTACCAGCTTAGACAGGGAGACAACTTTGAAGTGTG
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/db_xref="taxon:9606"
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/organism="Homo sapiens"
/organism="Homo sapiens"
/mol_type="mRNA"
/db_tref="taxon:9606"
/clone="IMAGE:5742198"
/tissue_type="medulla"
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/clone=lib="NIH_MGC_1198"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: brain; Vector brains medulla from anonymous male age 27. Library is oligo-df primed and directionally cloned (Ecoky site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."
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E i (bases 1 to 1067)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

C Contact: Robert Strausberg, Ph.D.

Email: cgapbe-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov

Plate: LLAM12759 row: p column: 07

High quality sequence stop: 761.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                      CAGTACTGCAATCACTGGCGAAATTTTGCTGACATTGATGATTCCTGGAAAAGTATAAAAG
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                                                                                                                                                                                                                                                                                                                      For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODIO67CE01QP1&c=10506.r.
Location/Qualifiers
1. .999
| organism="Homo sapiens" | multiple | mu
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Bmail: seqretefagenoscope.cns.fr, Web : www.genoscope.cns.fr web : sevagenoscope.cns.fr web : sevagenoscope.cns.fr web : sevagenoscope.cns.fr web : sevagenoscope.cns.fr web : serand cDNA was primed with a NotI-oligo(dT) primer end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a adivision of Invitrogen. This sequence belongs to sequence cluster
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              Score 915.8; DB 3;
Pred. No. 5.7e-263;
0; Mismatches 31;
              Query Match
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Best Local Similarity 96.4%;
Matches 1009; Conservative
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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1 (bases 1 to 1026)

1i,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length CDNA libraries and normalization
Unpublished (2001)
On Peb 16, 2001 this sequence version replaced
Contact: Genoscope
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                                     ACGNACTICTCTCAGGCTTTAACCGGG
                                                                                                                                                                                                                                                                                                                      AL577581.3 GI:46256603
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us-10-602-219-11.rst

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fcodon start=1
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Stonno, H., Akiyama, J., Nishi, K., Kteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yaujawke, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matrahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kavai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. SHEN integrated sequence analysis (RISA) system-384-format genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1376)
                                                                                                                                                                                                                                                                                                                                                                                                                                The FANTOM Consortium and the RIKEN Genome Exploration Research

    1286
    /note="unnamed protein product; galactosidase, alpha (MGD|MG1:1347344, GB|NM_013463, evidence: BLASTN, 99% match=1373)

                                                                                                                                                                                                                                                                                                 The RIKEN Genome Exploration Research Group Phase II Team and
                                                                                                                                                                                                                                                                                                                             FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 665-690 (2001)
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|db_xref="taxon:10090"
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    .1376
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URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
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HTC; CAP trapper.
Mus musculus (house mouse)
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Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
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                                                           657 AGCATTGTGTACTCCTGTGAGTGGCCTCTTTATATGTGGCCCTTTCAAAAGCCCAATTAT
                                                                                                                                                        GCTGGACCAGGGGGTTGGAATGACCCAGATATGTTAGTGATTGCAACTTTGGCCTCAGC
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                                                                                                                              ACAGAAATCCGACAGTACTGCAATCACTGGCGAAATTTTGCTGACATTGATGATTCCTGG
                                                                                                                                                                                                                                AAAAGTATAAAGAGTATCTTGGACTGGACATCTTTTAACCAGGAGAATTGTTGATGTT
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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AKO40081 2962 bp mRNA linear HTC 03-APR-2004 Mus musculus 0 day neonate thymus CDNA, RIKEN full-length enriched library, clone:A430057F16 product:galactosidase, alpha, full insert sequence.
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                      Greacacacacaccercresscratcarsscrececreceractearstcaacsarcre
                                                                                   CAAGACCCTTGGGCAAGCAGGCTACTGTTTCAGAAAGGAAAACCACATTGAGGTTTGG
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                                                            CGACACATCAGCCCTCAAGCTCTCCTTCAGGATAAGGACGTAATTGCCATCAAT
                                                                                                                                                                                                                                             CAGGACCCCTTGGGCAAGCAAACCTACCAGCTTAGACAGGGAGACAACTTTGAAGTGTGG
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muridae, Murinae, Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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PADWGVDLLKFDGCHCDSVVSLENGYKYMALALNRTGRSIVYSCEWPLYLRPFHKPNY
PIDQYYCHWANRPDDYDDSWESIKNILSWTVYYQKEIVVSAGPGSWNDPDMLVIGNFG
LSWDQQYTQWALWAINAAPLLMSNDILSWTVYQKEIVTAGPGSWNDPDMLVIGNFG
LSWDGWYDALMAINAAPLLMSNDLGSGGSGAKALLQNKDVIAINQDPLGKQGYCFR
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Lack for full-length cDNAs

Adachi, J. Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiracka, T., Hirozane, T., Ratoh, H., Kawai, J., Kojima, Y., Kondo, S., Konni, H., Kouda, M., Kagwa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konni, H., Kouda, M., Nishi, K., Nomura, K., Numazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, A., Shiraki, T., Salto, R., Sakai, C., Sakazume, N., Sano, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sakai, C., Sakai, K., Shiraki, T., Salto, R., Shiraki, T., Salto, R., Shiraki, T., Salto, R., Shiraki, T., Sakazume, N., Sayai, Y., Tagawi, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M. and Hayashizaki, Y., Towaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-UUL-2001) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN) Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reseggsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Physical and Theyson (E-mail:genome-reseggsc.riken.jp, Physical Bayashizaki, M. Phy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / LTAIN 1 AT 10 TO THE WANTELL SEPTITUCE LALUFWEIL GURALD MICHAEL FERMENTER MANTELL SEPTITUM GRAFFIELD GENERAL SEPTITUM GRAFFIELD GOREP DAG TESTITUM GRAFFIELD GOREP DAG TESTITUM GRAFFIELD GOREP DAG TESTITUM GRAFFIELD GOREP GOREP TESTITUM GRAFFIELD GOREP GOREP TESTITUM GOREP G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enriched mouse cDNA library"
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1. 2962

1. 2962

/organism="Mus musculus"
/mol_type="mRNR"
/strain="C57BL/6J"
/db_xref="Faxnr)"
/db_xref="taxnn:I0090"
/clone="A430057F16"
/clone="thymus"
/clone="thymus"
/clone="thymus"
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Mismatches 222;
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82.3%; Pred. No. 5.6
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/proteIn_id="BAC30508.1"
/db_xref="G1:26333581"
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Best Local Similarity 82.3
Matches 1033; Conservative
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EST 23-JUL-2004
                                                                                                                                                                                                                 741 GTTGGCCCTGAATAGGACTGGCAGAAGCATTGTGTTTTTCTTGTGAGTGGCCTCTCTATAT 682
                                                                                                                                                                                                                                                                                     Macaca mulatta (rhesus monkey)
Macaca mulatta
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      922 bp mRNA linear EST 23-JUL-2(ILLUMIGEN MCQ 24642 Katze MMLV Macaca mulatta cDNA clone IBIUW:23923 57 similar to Bases 5 to 920 highly similar to human CA45623 mRNA sequence.
CO645623 CO645623.1 GI:50567117
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                                                      TITIGGATACTACGACATIGATGCCCAGACCTITGCTGACTGGGGGAGTAGATCTGCTAAA
                                                                                                                          ATTTGATGGTGTTACTGTGACAGTTTGGAAATTTGGCAGATGGTTATAAGCACATGTC
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DEFINITION
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1 (bases I to 1133)
Magness, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B., Proll, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and Iadonato, S.P.
                                                                                                                            EST 23-JUL-2004
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                                                                                                                      CO645672
ILLUMIGEN MCQ 25513 Katze MMLV Macaca mulatta cDNA clone
IBIUW:23923 57 similar to Bases 27 to 1049 highly similar to human
GLA (Hs.69089), mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.03.05. 699 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               384 ACTGAAGCTAGGGATTTATGCAGATGTTGGAAATAAAACCTGCGCAGGCTTCCCTGGGAG 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="female" | /sex="female" | /dev_stage="adult" | /lab_host="Blectromax DH10B" | /clone lib="Katze_NMLV" | /note="Grgan: liver; Vector: pDONR 222; Site_1: BsrG 1; Site_2: BsrG 1; Created from CloneMiner cDNA_Library Construction kit (catalog #18249-029)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 981 GGGCGTTAGTGTTTTTTTTTTTTGAGGATTGCCAGTTAGCTAATTATGATAAACAAAGG
   264 CCTCTGCATTGATGACTGTTGGATGGCTCCCCAAAGAGATTCAGAAGGCAGACTTCAGGC
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Best Local Similarity 94.3%; Pred. No. 3.3e-255;
Matches 945; Conservative 0; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle,
Tel: 2063780400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORWARD: CCCTCACTAAAGGGAACAAA
BACKWARD: CACTATAGGGCGAATTGGGTA
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                                                                                                                                                                                                                                                Macaca mulatta (rhesus monkey)
Macaca mulatta
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CO645672.1 GI:50567166
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PCR PRimers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 1071)

2. Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Pull-length cDNA libraries and normalization

1. (Dases 1 to 1071)

2. Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Pull-length cDNA libraries and normalization

3. Discourage contact: Genoscope

Contact: Genoscope

Genoscope - Centre National de Sequencage

Genoscope - Centre National de Sequencage

Contact: Genoscope

Genoscope - Centre National de Sequencage

Genoscope - Centre National de Sequencage

anil: segrefégenoscope.cns.fr

Email: segrefégenoscope.cns.fr

Estrand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and Econe V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster
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AL575861
AL575861
R1575861.3 GI:46248771
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                                                                                                                             GCAGATGGTTATAAGCACATGTCCTTGGCCCTGAATAGGACTGGCAGAAGCATTGTGTAC
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                      ACCIGCGCAGGCTTCCCTGGGAGTTTTGGATACTACGACATTGATGCCCAGACCTTTGCT
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/clone="IBIUW:23923"

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/clone lib="Katze MMLV"

/note="Organ: liver; Vector: pDONR 222; Site_1: BsrG I;

Site_2: BsrG I; Created from CloneMiner cDNA Library

Construction kit (catalog #18249-029)"
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                                                                                                                                                                                                                                                                                Fax: 2063780408
Baall: emagnesseallumigen.com
Sequenced on 2004.03.02. 796 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Hilumigen Blosciences Inc. For further information, see
http://www.macaque.org
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Cercopithecidae; Cercopithecinae; Macaca.
1 (bases 1 to 922)
Magness, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B.,
Proll, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G.
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                                                                                                                                                                                      Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle,
Tel: 2063780400
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Insert Length: 922 Std Bror: 0.00
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POLYA-No.
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/tissue type="PLACENTA COT 25-NORWALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORWALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                                                            GCAGGCTTCCCTGGGAGTTTTGGATACTACGACATTGATGCCCCAGACCTTTGCTGACTGG
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                                                                                                 ch 69.6%; Score 880.8; DB 1; Il Similarity 91.6%; Pred, No. 1.9e-252; 985; Conservative 20; Mismatches 61;
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1086	175	1146	115	1206	55	
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2. /cgn2_6/ptodata/1/ina/5_COMB.seq:*

3. /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4. /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

5. /cgn2_6/ptodata/1/ina/RD_COMB.seq:*

6. /cgn2_6/ptodata/1/ina/RD_COMB.seq:*

7. /cgn2_6/ptodata/1/ina/RD_COMB.seq:*

8. /cgn2_6/ptodata/1/ina/RD_COMB.seq:*

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	Description	Sequence 11, Appl	11,	13,	13,	7, 1	7,	Seguence 3, Appli	'n	ď	6	'n	'n	18	18,	Sequence 3, Appli	Sequence 18, Appl	٦,	7	6, 4	15,	Sequence 15, Appl	17,	17,	77
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TYPE: DNA
ORGANISM: Homo sapiens
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RESULT 2 US-10-103-327-11 ; Sequence 11, Application US/10103327

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GENERAL INFORMATION:

APPLICANT: GARGER, Stephen A.

APPLICANT: TUREEN, Thomas H.

APPLICANT: KUMAGAI, Monto H.

TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION FILE REFERENCE: 008010087CPUS06

CURRENT FILING DATE: 2002-20

PRIOR APPLICATION NUMBER: 205/993,059

PRIOR PILING DATE: 2001-11-13

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastESC for Windows Version 4.0 Z ö DB 3; Query Match
100.0%; Score 1266;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1266; Conservative 0; Mismatches 601 661 g 8

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US-09-993-059-13
is Sequence 13, Application US/09993059
is Batent No. 6807696
is General Information:
is APPLICANT: GARGER, Stephen A.
is APPLICANT: TURBEN, Thomas H.
is APPLICANT: TURBEN, Monto H.
is TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
is TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
is TILLE REFERENCE: 0.08010087CPUS06
is CURRENT APPLICATION NUMBER: US/09/993,059
is CURRENT APPLICATION NUMBER: 2001-11-13
is NUMBER OF SEQ ID NOS: 37
is SOFTWARE: FastSEQ for Windows Version 4.0
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; NAME/KEY: CDS
; LOCATION: (1)...(1284)
US-09-993-059-13
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Patent No. 6887696;
GENERAL INFORMATION:
APPLICANT: GARGER, Stephen A.
APPLICANT: TURPEN, Thomas H.
APPLICANT: KUNAGAI, Monto H.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
CURRENT APPLICATION NUMBER: US/09/993,059;
CURRENT APPLICATION NUMBER: US/09/993,059
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                                                                                                               TCAAGGTTAAGAAGTCACATAAATCCCACAGGCACTGTTTTGCTTCAGCTAGAAAACACA
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                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/10103327

Patent No. 6890748

GENERAL INFORMATION:
APPLICANT: TUREN, Stephen A.
APPLICANT: TUREN, Thomas H.
APPLICANT: TUREN, Thomas H.
TITLE OF INVENITON: PRODUCTION OF LYSOSOMAL ENZYMES IN TITLE OF INVENITON: PRODUCTION OF LYSOSOMAL ENZYMES IN TITLE OF INVENITON: PRODUCTION OF LYSOSOMAL ENZYMES IN TITLE OF INVENITON: PRODUCTION OF CURRENT APPLICATION NUMBER: US/10/103,327
CURRENT APPLICATION NUMBER: US/09/993,059
PRIOR APPLICATION NUMBER: US/09/993,059
PRIOR FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 1284
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1264; Conservative 0; Mismatches
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; LOCATION: (1) ... (1284)
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                                                                                                            961 CAGGACCCTTGGGCAAGCAAGGGTACCAGCTTAGACAGGGAGACAACTTTGAAGTGTGG
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841 GTAACTCAGATGGCCCTCTGGGCTATCATGGCTGCTCCTTTATTCATGTCTAATGACCTC
                                              901 GGACACATCAGCCCTCAAGCCAAAGCTCTCCTTCAGGATAAGGACGTAATTGCCATCAAT
                                                                                             961 CAGGACCCCTTGGGCAAGCAAGGGTACCAGCTTAGACAGGGAGACAACTTTGAAGTGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/10103327

Patent No. 6890748

GENERAL INFORMATION:
APPLICANT: GARGER, Stephen A.
APPLICANT: TURPEN, Thomas H.
TITLE OF INVENTION: PRODUCTION OF LYSOSOWAL ENZYMES IN
TITLE OF INVENTION: PRODUCTION OF LYSOSOWAL ENZYMES IN
TITLE OF INVENTION: PRODUCTION OF LYSOSOWAL ENZYMES IN
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
FILE REFERENCE: 008010087CPUS06
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: US/09/993,059
PRIOR FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Homo sapiens
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; LOCATION: (1)...(1275)
US-10-103-327-7
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                                                                                                                                                                                                               1; Indels
                                                                                                                                                                            ; Score 1263.4;
; Pred. No. 0;
0; Mismatches
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 7
                                                                                                                                                                              Query Match
Best Local Similarity 99.9%;
Matches 1264; Conservative
                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                             ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1275)
US-09-993-059-7
                                                  LENGTH: 1278
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Patent No. 6887666;
GENERAL INFORMATION:
APPLICANT: GARGER, Stephen A.
APPLICANT: TURPEN, Thomas H.
APPLICANT: KUMAGAI, Monto H.
TITLE OF INVENTION: PRODUCTION OF LYSOSOWAL ENZYMES IN TITLE OF INVENTION: PRANTS ENTANCE IN FILE REFERENCE: 008010087CPUS06;
CURRENT APPLICATION NUMBER: US/09/993,059;
CURRENT FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PASISEC for Windows Version 4.0
SEQ ID NO 3.
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; Patent No. 6890748
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: TURBEN, Thomas H.
; APPLICANT: TURBEN, Thomas H.
; TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
; TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
; TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
; TITLE OF INVENTION: PLANTS BY 1200-00-00
; TITLE OF INVENTION: PLANTS BY 1200-00-00
; TITLE OF INVENTION: PLANTS BY 1200-00-00
; TITLE OF INVENTION NUMBER: US/10/103,327
; CURRENT FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FASTED FOR Windows Version 4.0
; SEQ ID NO 3.30
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	1201 TCAAGGTTAAGAAGTCACATAAATCCCACAGGCACTGTTTGCTTCAGCTAGAAAACACA 126 1201 TCAAGGTTAAGAAGTCAAAATCCCACAGGCACTGTTTTGCTTCAGCTAGAAAACACA 126 1201 TCAAGGTTAAGAAGTCACATAAATCCCACAGGCACTGTTTTGCTTCAGCTAGAAAAACACA 126	Oy 1261 ATGTA 1265 Db 1261 ATGCA 1265	RESULT 9 US-09-993-059-9 . Seminare 9 annication IIS/A9991A59	; Patent No. 6887656 ; GENERAL INFORMATION: ; APPLICANT; GRAGER, Stephen A.	; APPLICANT: KUNGEN; INORES; AND TO THE OF INVENTION: PLANSIENT EXPRESSION ; TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION ; TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION	FILE KEFERRACE: 008010087CPUSU6; CURRENT APPLICATION NUMBER 10S/09/993,059; CURRENT FILING DATE: 2001-11-13; NUMBER OF SEQ ID NOS: 37	; SOFTHWAKE: FASTSEQ FOR WINGOWS VERSION 4.0 ; SEQ ID NO 9 ; LENGTH: 1296 ; TYBS: DNA	; UNCADISM: HOMO BADIENS ; FEATURE: ; NAME/KEY: CDS ; LOCATION: (1)(1296) US-09-993-059-9	Query Match 99.8%; Score 1263.4; DB 3; Length 1296; Best Local Similarity 99.9%; Pred. No. 0; Matches 1264; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		61 CTCGTTTCCTGGGACATCCCTGGGGCTAGACACTGGACAATGGATTGGCAAGACGCCT	Qy 121 ACCATGGGTGGCTGCACTGGGAGGCGCTTCATGTGCAACCTTGACTGCCAGGAAGAGCCA 180 Db 121 ACCATGGGTGGCTGCACTGGGAAGGGCTTCATGTGCAACCTTGACTGCCAGGAAGAGCCA 180	Qy 181 GATTCCTGCATCAGTGAAAGCTCTTCATGGAGATGGCAGGTCATGGTCTCAGAAGGC 240	OY 241 TGGAAGGATGCAGGTTATGAGTACCTCTGCATTGATGACTGTTGGATGGCTCCCCAAAGA 300	Qy 301 GATTCAGAAGGCAGACTTCAGGCAGACCTCAGGGCTTTCCTCATGGGATTCGCCAGCTA 360

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                  CAGGACCCCTTGGGCAAGCAAGGGTACCAGCTTAGACAGGGAGACAACTTTGAAGTGTGG
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US-09-991-059-5
; Sequence 5, Application US/09993059
; Patent NO. 6887696
; GENERAL INFORMATION:
; APPLICANT: GARGER, Stephen A.
; APPLICANT: TURPEN, Thomas H.
; APPLICANT: TURPEN, Thomas H.
; TITLE OF INVENTION: PRODUCTION OF LYSOSOWAL ENZYMES IN
; TITLE OF INVENTION: PRODUCTION OF LYSOSOWAL ENZYMES IN
; TITLE OF INVENTION: PRODUCTION OF LYSOSOWAL ENZYMES
; TITLE OF INVENTION: PRODUCTION OF LYSOSOWAL ENZYMES
; TITLE OF INVENTION: PLANSIENT EXPRESSION
; FILE REFERENCE: 008010087CPUSO6
; CURRENT APPLICATION NUMBER: US/09/993,059
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FABELSEQ for Windows Version 4.0
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Matches 1264; Conservative
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
FILE REFERENCE: 008010087CPUS06
CURRENT APPLICATION NUMBER: US/10/103,327
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: US/09/993,059
PRIOR FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FRAESEQ FOR Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                             99.9%; Score 1263.4;
99.9%; Pred. No. 0;
ive 0; Mismatches
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Best Local Similarity 99.9
Matches 1264, Conservative
                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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; LOCATION: (1)...(1296)
US-10-103-327-9
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US-10-103-327-5

j Sequence 5, Application US/10103327

patent No. 680748

GENERAL INFORMATION:
APPLICANT: GARGER, Stephen A.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION FILE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION FILE OF INVENTION: PLANTS BY SALICATION OF LYSOSOMAL ENZYMES IN TITLE OF INVENTION: PLANTS BY SALICATION OF LYSOSOMAL ENZYMES IN TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION CURRENT FILING DATE: 2002-03-20

PRIOR APPLICATION NUMBER: US/09/993,059

PRIOR APPLICATION NUMBER: US/09/993,059

PRIOR PILING DATE: 2001-11-13

NUMBER OF SEQ ID NOS: 37
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Best Local Similarity 99.9
Matches 1264; Conservative
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
FILING DATE:
FLING DATE:
CLASSIFICATION: 435
ATTORNEY/AGBNT INFORMATION:
NAME: Fraer, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/003001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION
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Matches 1263; Conservative
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US-08-928-881-18
; Sequence 18, Application US/08928881
; Patent No. 6083725
; GENERAL INFORMATION:
; APPLICANT: Selden et al., Richard F.
; TITLE OF INVENTION: DEFICIENCY
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COMPUTER READABLE FORM:
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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07236/003001
                                                                                                                                                                                                                           99.7%; Score 1261.8;
99.8%; Pred. No. 0;
:ive 0; Mismatches
                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
JOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-543-921-18
         TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1343 base_pairs
 REFERENCE/DOCKET NUMBER:
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Best Local Similarity 99.8
Matches 1263; Conservative
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                                    756 AGTATCTTGGACTGGACATCTTTTAACCAGGAGAATTGTTGATGTTGCTGGACCAGGG
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                                                                                     GGTTGGAATGACCCAGATATGTTAGTGATTGGCAACTTTGGCCTCAGCTGGAATCAGCAA
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CORESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
COUNTRY: USA
CONPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PISP FC compatible
OPERATIG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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US-09-541-921-18
is Sequence 18, Application US/09543921
j Patent No. 6395884
is GENERAL INFORMATION:
it APPLICANT: Selden et al., Richard F.
it TIE OF INVENTION: THERAPY FOR ALPHA-GALACTOSIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,921
PILING DATE: 06-Apr-2000
CLASSIPICATION: <universely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
PAPPLICATION NUMBER: 08/928,881
FILING DATE: «UNKnown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
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1	NESULT 15 US-09-266-014-3 15 Sequence 3, Application US/09266014 16 Patent No. 6458574 17 Application US/09266014 18 Patent No. 6458574 18 Sequence 3, Application US/09266014 18 APPLICANT: Selden, Richard F 19 APPLICANT: Selden, Richard F 10 APPLICANT: Milliams, Melanie D 10 APPLICANT: Milliams, Melanie D 10 APPLICANT: Daniel, Peter (Inc. alpha-Galactosidase A Deficiency FILE REFERENCE: FABRY DISABE (18082-00.1) 10 CURRENT PAPLICATION NUMBER: 00/026,041 11 PRIOR PILING DATE: 1999-03-11 12 PRIOR PILING DATE: 1999-03-11 13 PRIOR PILING DATE: 1999-03-11 14 PRIOR PILING DATE: 1999-03-12 15 PRIOR APPLICATION NUMBER: 00/026,041 16 PRIOR APPLICATION NUMBER: 00/026,041 17 PRIOR PARICALION NUMBER: 00/026,041 18 PRIOR PILING DATE: 1999-03-12 19 PRIOR APPLICATION NUMBER: 00/026,041 19 PRIOR APPLICATION NUMBER: 00/026,041 10 PRIOR APPLICATION NUMBER: 00/026,041 10 PRIOR APPLICATION NUMBER: 00/026,041 11 PRIOR APPLICATION NUMBER: 00/026,041 12 PRIOR APPLICATION NUMBER: 00/026,041 13 PRIOR APPLICATION NUMBER: 00/026,041 14 PRIOR APPLICATION NUMBER: 00/026,041 15 PRIOR APPLICATION NUMBER: 00/026,041 16 PRIOR APPLICATION NUMBER: 00/026,041 17 PRIOR APPLICATION NUMBER: 00/026,041 18 PRIOR APPLICATION NUMBER: 00/026,041 19 PRIOR APPLICATION NUMBER: 00/026,041 10 PRIOR APPLICATION NUMBER: 00/026,041 10 PRIOR APPLICATION NUMBER: 00/026,041 10 PRIOR APPLICATION NUMBER: 00/026,041 11 PRIOR APPLICATION NUMBER: 00/026,041 12 PRIOR APPLICATION NUMBER: 00/026,041 13 PRIOR APPLICATION NUMBER: 00/026,041 14 PRIOR APPLICATION NUMBER: 00/026,041 15 PRIOR APPLICATION NUMBER: 00/026,041 16 PRIOR APPLICATION NUMBER: 00/026,041 17 PRIOR APPLICATION NUMBER: 00/026,041 18 PRIOR APPLICATION NUMBER: 00/026,041 18 PRIOR APPLICATION NUMBER: 00/026,041 19 PRIOR APPLICATION NUMBER: 00/026,041 19 PRIOR APPLICATION NUMBER: 00/026,041 10 PRIOR APPLICATION NUMBER: 00/026,041 10 PRIOR APPLICATION NUMBER: 00/026,041 11 PRIOR APPLICATION NUMBER: 00/026,041 11 PRIOR APPLICATION NUMBER: 00/026,041 12 PRIOR A

Search completed: December 26, 2005, 08:34:32 Job time: 268 secs

1261 ATGTA 1265 ||| | 1296 ATGCA 1300

Sequence Sequence Sequence

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US-10-984-389-3
US-00-103-3-059-9
US-10-602-219-9
US-10-602-219-9
US-10-984-389-9
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US-10-103-3-059-5
US-10-103-3-059-5
US-10-602-219-5
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Sequence Seq

ALIGNMENTS

Sequence

RESULT 1
US-09-993-059-11
US-09-993-059-11
Sequence 11, Application US/09993059
Publication No. US20020088024A1
GENERAL INFORMATION:
APPLICANT: GARGER, Stephen A.
APPLICANT: GARGER, Thomas H.
TITLE OF INVENTION: PRODUCTION OF LYSOSOWAL ENZYMES IN
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
FILE REFERENCE: 008010087CPU366
CURRENT APPLICATION NUMBER: US/09/993,059
CURRENT FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 1266
TYPE: DNA
ORGANISM: Homo sapiens
PATURES
LOCATION: (1)...(1266)
US-09-993-059-11
OLGATON: (1)...(1266)

Query Match 100.0%; Score 1266; DB 3; Length 1266; Best Local Similarity 100.0%; Pred. No. 0; Matches 1266; Conservative 0; Mismatches 0; Indels 0; Gaps

Sequence Sequence Sequence

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Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 2 Sequence 7 Sequence 7 Sequence 7 Sequence 7 Sequence 3 Sequence 3

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1 atgcagctgaggaacccaga.....agctagaaaacacaatgtaa 1266 Published Applications NA Main:*

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9: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCONB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCONB.seq:* Total number of hits satisfying chosen parameters: 9793542 seqs, 4134689005 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries IDENTITY_NUC Gapop 10.0 , Gapext 1.0 nucleic search, using December 26, 2005, seq length: 0 seq length: 200000000 US-10-602-219-11 1266 Copyright Scoring table: Title: Perfect score: Minimum DB Maximum DB OM nucleic Sequence: Searched: Database 6 Run

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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S	US-09-993-059-111 US-09-993-059-111 US-10-602-220-111 US-10-802-220-111 US-10-984-388-111 US-10-993-059-113 US-10-993-059-113 US-10-103-327-13 US-10-802-19-13 US-10-802-19-13 US-10-984-388-13 US-10-984-389-13 US-10-802-220-7 US-10-802-230-7 US-10-802-230-7 US-10-802-230-7 US-10-984-388-7 US-10-984-388-7 US-10-984-388-7 US-10-984-388-7 US-10-984-388-7 US-10-983-059-3 US-10-103-327-3 US-10-602-220-3 US-10-602-220-3 US-10-802-239-3 US-10-802-239-3 US-10-802-239-3 US-10-802-239-3 US-10-802-239-3 US-10-802-239-3 US-10-802-239-3 US-10-802-239-3 US-10-802-239-3 US-10-802-239-3 US-10-802-239-3 US-10-802-239-3
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Sequence 11, Application US/10103327

Publication No. US20030106095A1

GENERAL INFORMATION:
APPLICANT: TURPEN, Stephen A.
APPLICANT: TURPEN, Thomas H.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
CURRENT PEPLICATION NUMBER: US/10/103,327
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: US/09/993,059

PRIOR FILING DATE: 2001-11-13
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100.0%; Pred. No. 0;
ive 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 1266; Conservative
                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: CDS
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US-10-103-327-11
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PRIOR FILING DATE: 1992-07-31
PRIOR APPLICATION NUMBER: 07/600,244
PRIOR FILING DATE: 1990-10-22
PRIOR FILING DATE: 1990-10-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER: OF SEQ ID NOS: 32
SOFTMARE: Patentin version 3.2
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APPLICANT: LARGE Scale Biology Corporation
APPLICANT: Larges Scale Biology Corporation
APPLICANT: Larges Gregory P.
APPLICANT: Evain, Robert L.
APPLICANT: Evain, Robert L.
APPLICANT: Expired Gregory P.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN PLANTENT EXPRESSION
FILE REPERENCE: LSBC-0003-06-23
CURRENT APPLICATION NUMBER: 09/93,059
PRIOR PELLING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/266,127
PRIOR PELLING DATE: 2000-07-26
PRIOR PELLING DATE: 1999-05-21
PRIOR PELLING DATE: 1999-12-29
PRIOR PELLING DATE: 1994-10-14
PRIOR PLILING DATE: 1993-12-30
PRIOR PELLING DATE: 1994-10-14
PRIOR PELLING DATE: 1994-01-19
PRIOR APPLICATION NUMBER: 07/923,692
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GENERAL INFORMATION:
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GENERAL INCORPATION:
APPLICANT: Turpen, Thomas H.
APPLICANT: Turpen, Thomas H.
APPLICANT: Turpen, Thomas H.
APPLICANT: Ewin, Robert L.
APPLICANT: Ewin, Robert L.
APPLICANT: Erwin, Robert L.
APPLICANT: Or INVERVION: PRODUCTION OF LYSOSOMAL ENZYMES IN PLANTS BY TRANIENT FILE REFERENCE: LSBC-0087-CP07B
CURRENT FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 08/116,572
PRIOR APPLICATION NUMBER: 08/116,414
PRIOR FILING DATE: 1991-10-30
PRIOR FILING DATE: 1991-12-30
PRIOR APPLICATION NUMBER: 07/997,733
PRIOR FILING DATE: 1992-10-30
PRIOR APPLICATION NUMBER: 07/997,733
PRIOR FILING DATE: 1992-07-31
PRIOR FILING DATE: 1992-07-31
PRIOR FILING DATE: 1992-07-31
PRIOR FILING DATE: 1990-10-22
PRIOR FILING DATE: 1990-10-22
PRIOR FILING DATE: 1991-01-16
PRIOR PRIOR APPLICATION NUMBER: 07/600,244
PRIOR FILING DATE: 1991-01-16
PRIOR PLING DATE: 1991-01-16
PRIOR PLING DATE: 1991-01-16
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US-10-851-388-11
i Sequence 11, Application US/10851388
i Publication No. US20040234516A1
i GENERAL INFORMATION:
APPLICANT: GARGER, Stephen A.
APPLICANT: TUREN, Thomas H.
APPLICANT: TUNENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION FILE REFERENCE: 008010087CPUS06
CURRENT FILING DATE: 2004-05-21
PRIOR APPLICATION NUMBER: US/09/993,059
PRIOR FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FRASESQ for Windows Version 4.0
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ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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ORGANISM: Homo sapiens
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; NAME/KEY: CDS
; LOCATION: (1)...(1266)
US-10-851-388-11
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Publication No. US20020088024A1
GENERAL INFORMATION:
APPLICANT: GANGER, Stephen A.
APPLICANT: TURPEN, Thomas H.
APPLICANT: KUMAGAI, Monto H.
TITLE OF INVENTION: PRODUCTION OF LYSOSOWAL ENZYMES IN TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION;
FILE REFERENCE: 008010087CPUS06
CURRENT APPLICATION NUMBER: US/09/993,059;
CURRENT FILING DATE: 2001-11-13
CURRENT FILING DATE: 2001-11-13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1264; Conservative 0; Mismatches
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ORGANISM: Homo sapiens
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Sequence 11, Application US/10984389;
Publication No. US20050125859A1
GENERAL INFORMATION:
APPLICANT: GARGER, Stephen A.
APPLICANT: TURBEN, Thomas H.
APPLICANT: TURBEN, THOMAS H.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION; FILE REFERENCE: 008010087CPUS06; CURRENT FILING DATE: 20810087CPUS06; CURRENT FILING DATE: 2001-11-08; PRIOR APPLICATION NUMBER: US/09/993,059; PRIOR FILING DATE: 2001-11-13; NUMBER OF SEQ ID NOS: 37; SOFTWARE: FastSEQ for Windows Version 4.0; LENGTH: 1266
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100.0%; Score 1266;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1266; Conservative 0; Mismatches
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ORGANISM: Homo sapiens
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; LOCATION: (1)...(1266)
US-10-984-389-11
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99.8%; Score 1264; L
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1264; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/10/602,219
CURRENT FILING DATE: 2003-06-23
PRIOR APPLICATION NUMBER: 09/993,059
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-07-26
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-10-14
PRIOR FILING DATE: 1994-10-14
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PRIOR FILING DATE: 1994-10-19
PRIOR FILING DATE: 1993-12-29
PRIOR FILING DATE: 1993-12-30
PRIOR FILING DATE: 1994-01-19
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Publication No. US20040016021A1
GENERAL INFORMATION:
APPLICANT: Large Scale Biology Corporation
APPLICANT: Turpen, Thomas H.
APPLICANT: Pogue, Gregory P.
APPLICANT: Erwin, Robert L.
APPLICANT: Grill, Laurence K.
TITLE OF INVENTION: RROBUCTION OF LYSOSOMAL ENZYMES IN PLANTS IF ILE REFERENCE: LSBC-0087-CP09B
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PRIOR FILING DATE: 1994-10-14

PRIOR APPLICATION NUMBER: 08176,414

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PRIOR FILING DATE: 1994-00-13

PRIOR FILING DATE: 1994-00-13

PRIOR FILING DATE: 1990-10-22

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PRIOR PRIOR APPLICATION NUMBER: 07/600,244

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PRIOR PILING DATE: 1991-01-16

PRIOR PILING DATE: 1991-01-16

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin version 3.2

SEQ ID NOS: 32
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Best Local Similarity 100.0*; Pred. No. 0;
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Sequence 13, Application US/1060220

Publication No. US20040023281A1

GENERAL INPORMATION:

APPLICANT: Turpen, Thomas H.

APPLICANT: Evain, Monto H.

APPLICANT: Evain, Monto H.

APPLICANT: Evain, Robert L.

APPLICANT: Evain, Robert L.

APPLICANT: Bogue Gregory P.

APPLICANT: Brain, Robert L.

APPLICANT: Brain Robert L.

APPLICANT: Brain Robert L.

APPLICANT: Brain Robert L.

APPLICANT: Brain Robert L.

APPLICATION NUMBER: 09/933,059

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PRIOR APPLICATION NUMBER: 09/316,572

PRIOR FILING DATE: 1999-05-21

PRIOR APPLICATION NUMBER: 09/324,003
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| Publication No. US20040234516A1
| GENERAL INFORMATION: US20040234516A1
| APPLICANT: TURPEN, Thomas H. APPLICANT: TURPEN, Thomas H. APPLICANT: KUMAGAI, Monto H. TITLE OF INVENTION: PRODUCTION OF LYSOSOWAL ENZYMES IN TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION FILE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION CURRENT APPLICATION NUMBER: US/10/891,388 CURRENT APPLICATION NUMBER: US/10/993,059
| PRIOR FILING DATE: 2001-11-13 NUMBER OF SEQ ID NOS: 37
| SOFTWARE: FastSEQ for Windows Version 4.0 | SEQ ID NO! 1284
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99.8%; Score 1264; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1264; Conservative 0; Mismatches
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ORGANISM: Homo sapiens
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Publication No. US20020088024A1
GENERAL INFORMATION:
APPLICANT: GARGER, Stephen A.
APPLICANT: TURPEN, Thomas H.
APPLICANT: KUMAGAI, Monto H.
ITILE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
FILE REPERENCE: 008010087CPUS06
CURRENT APPLICATION NUMBER: US/09/993,059
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Publication No. US20050125859A1
GENERAL INFORMATION:
APPLICANT: GRACER, Stephen A.
APPLICANT: TURPEN, Thomas H.
APPLICANT: KUMAGAI, Monto H.
ITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
ITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
ITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
CURRENT APPLICATION NUMBER: US/10/984,389
CURRENT FILING DATE: 2004-11-08
FRIOR FILING DATE: 2004-11-13
NUMBER OF SEQ ID NOS: 37
SEQ ID NO 13
LENGTH: 1284
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ORGANISM: Homo sapiens
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99.9%; Pred. No. 0;
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Best Local Similarity 99.9
Matches 1264; Conservative
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ORGANISM: Homo sapiens
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US-10-103-327-7
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0; Mismatches
 CURRENT FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 1278
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Best Local Similarity 99.9%;
Matches 1264; Conservative
                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
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BY TRANIENT EXPRESSION
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                                                                                                                                                                                                 GENERAL INVEXMATION:
APPLICANT: Large Scale Biology Corporation
APPLICANT: Turpen, Thomas H.
APPLICANT: Purpen, Thomas H.
APPLICANT: Purpen, Thomas H.
APPLICANT: Erwin, Robert L.
ITILE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN PLANTS BY TRANIENT FILE REFERENCE: LSBC-003-CP09B
CURRENT FILING DATE: 2003-06-23
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/993,059
PRIOR PRILING DATE: 2000-07-26
PRIOR PELLOR DATE: 1999-05-21
PRIOR PELLOR DATE: 1999-05-31
PRIOR PELLOR DATE: 1999-05-31
PRIOR PELLOR DATE: 1999-10-14
PRIOR PELLOR DATE: 1999-10-19
PRIOR PELLOR DATE: 1999-10-22
PRIOR PELLOR DATE: 1999-10-19
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Pred. No. 0;
0; Mismatches
                                                                                                                                            Sequence 7, Application US/10602219; Publication No. US20040016021A1; GENERAL INFORMATION:
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(c) 1993 - 2005 Compugen Ltd
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seq length: 200000000
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Sequence 64685, A Sequence 121, App Sequence 1317, App Sequence 13493, A Sequence 42925, A Sequence 66, Appl Sequence 13227, A Sequence 13227, A Sequence 13227, A Sequence 13271, A Sequence 54, Appl Sequence 56, Appl Sequence 57062, A Sequence 57

US-10-750-185-64685
US-10-331-826A-121
US-10-821-23-4-3-7
US-10-995-54302
US-10-995-561-13493
US-10-750-185-54302
US-10-750-185-39400
US-11-121-086-60
US-11-121-086-60
US-11-121-086-61
US-10-195-561-1327
US-10-995-561-1327
US-10-995-261-1327
US-10-750-185-39502
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US-10-509-921-6
US-10-509-921-6

ALIGNMENTS

Sequence 1

RESULT 2 US-10-750-185-42255 ; Sequence 42255, Application US/10750185

28311, A 61883, A 37071, A 3, Appli

Sequence Sequence

US-11-121-086-12 US-11-121-086-75 US-10-750-185-37196 US-10-750-185-28311 US-10-750-185-61883 US-10-750-185-61883 US-10-750-185-61883

1522 854 1084 1783 168516

Sequence 149, Appl Sequence 68, Appl Sequence 23, Appl Sequence 53897, A Sequence 13246, A Sequence 29504, A Sequence 29504, A Sequence 29506, A Sequence 3186, A Sequence 12, Appl Sequence 12, Appl Sequence 75, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl

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Sequence 55363, A Sequence 43877, A Sequence 68, App Sequence 69, App Sequence 69, Appl Sequence 69, Appl Sequence 13246, A

US-10-750-185-42255 US-10-995-561-13204 US-10-750-185-43837 US-10-750-185-43837 US-10-821-234-149 US-11-121-086-68 US-11-121-086-69 US-11-121-086-69 US-10-750-185-53897 US-10-750-185-53897 US-10-750-185-529100 US-10-995-561-13246 US-10-995-561-13246 US-10-750-185-60200 US-10-995-61-13286

Sequence 40681, A Sequence 42255, A Sequence 13204, A Sequence 53363, A

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Length

Query

Published Applications NA New:*

1: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

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Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Post-processing:

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                                                                                                                                     301257 AGCAGAAĞCTCAACCAĞCAĞCTGTCAAAĞATCTĞCAĞGTĞCACTĞGĞGACTGGĞC 301203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.7%; Score 34; DB 6; Length 1932; Best Local Similarity 57.5%; Pred. No. 0.7; Matches 61; Conservative 0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: WAILIOO-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR PAPLICATION NUMBER: US 60/437,482
PRIOR PILING DATE: 2002-12-31
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
PILE REFERENCE: MMI1100-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 43877
LENGTH: 1437
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Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MI GENOMICS, INC.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                              ; Sequence 55363, Application US/10750185; Publication No. US20050260603A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Bovine 19866880928582
US-10-750-185-55363
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                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICATY: MAI GENOMICS, INC.
APPLICANT: BERR, Richard
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, TOM
APPLICANT: BATES, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 55363
LENGTH: 1932
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; ORGANISM: Bovin
US-10-750-185-43877
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; CTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     975 CAAGCAAGGGTACCAGCTTAGACAGGGAGACAACTTTGAAGTGTGGGAACGACCTCTCTC 1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-995-561-13204/c
Sequence 13204, Application US/10995561
Sequence 13204, Application US/10995561
Sequence 13204, Application Wo. US20050272054A1
SEQUENCE INCORNATION
TITLE OF INVENTION GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCUAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT APPLICATION NUMBER: US/10/995,561
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 321019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   915 TCAAGCCAAAGCTCTCCTTCAGGATAAGGACGTAATTGCCATCAAGGACCCCTTGGG 974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                          JUNEARALIONIE, SUE K.

JAPPLICANT: DENISE, SUE K.

JAPPLICANT: EDENISE, SUE K.

JAPPLICANT: RERR, Richard

JAPPLICANT: ROSENFELD, David

APPLICANT: ROSENFELD,

APPLICANT: ROSENFELD,

APPLICANT: BATES, Stephen

APPLICANT: BATES, Stephen

JAPPLICANT: RATION DENISE

TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MMI1100-2

CURRENT APPLICATION NUMBER: US 60/437, 482

PRIOR FILING DATE: 2002-12-31

PRIOR FILING DATE: 2002-12-31

NUMBER OF SEQ ID NOS: 64922

SOFTWARE: PALENTIN VERSION 3.1

SEQ ID NO 42255

LENGTH: 1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ougry Match
2.9%; Score 36.6; DB 6; Length 1306;
Best Local Similarity 53.1%; Pred. No. 0.067;
Matches 78; Conservative 0; Mismatches 69; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; OPGANISM: Bovine 19866880955804
US-10-750-185-42255
  Publication No. US20050260603A1
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NAME/KEY: misc feature
LOCATION: (1)...(321019
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US-11-121-086-69
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; Sequence 149, Application US/10821234
; Sequence 149, Application US/10821234
; GENERAL INFORMATION:
    APPLICANT: Labat, Ivan
    APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/00/462,047
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR PILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 149
: LENTH: 1666
                                                                                                          835 CAGCAAGTAACTCAGAIGGCCCTCTGGGCTAICAIGGCTGCTCTTTAITCAIGTCTAAI 894
                                                                                                                                                         458 CAGGAATTTATTGGGTTGGCTGACTGGGATATCCAGGGAGGAGGCTGGCCTCAGGAATTCA 399
                                                                                                                                                                                                                                                           398 gagcccagagccrrcrgccrccrcrcrcrcrcrccgrgracragargercrifiga 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 CAACCTIGACTGCCAGGAAGAGCCAGATTCCTGCATCAGTGAGAAGCTCTTCATGGAGAT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 CAGTCTTGCCTCCCTGGAATACTCCGATTACTCCAAATGTAAAAAGATCATGATTGAGAG 297
                                                                                                                                                                                                             895 GACCTCCGACACATCAGCCCTCAAGCCCAAAGCTCTCCTTCAGGATAAGGACGTAATTGCC 954
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; Sequence 68, Application US/11121086
; Sequence 68, Application US/11121086
; Publication No. US20850266459A1
; GENERAL INFORMATION:
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFRENCE: 09138-6000-00000
; CURRENT TILING DATE: 2006-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 68
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Query Match 2.6%; Score 33; DB 6; Length 1437; Best Local Similarity 53.5%; Pred. No. 1.3; Matches 69; Conservative 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 2.6%; Score 32.8; DB 6; Length 10 Best Local Similarity 64.5%; Pred. No. 1.6; Matches 49; Conservative 0; Mismatches 27; Indels
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                                                                                                                                                                                                                                                                                                                     955 ATCAATCAG 963
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ORGANISM: Homo sapiens
US-11-121-086-68
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ORGANISM: Homo sapiens
US-10-821-234-149
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134039 ATTACACGCATATGCCAAAGTACTAGGCTCACTTGCTAATTTTAGCACCCAATGATGT 134098
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                                                                                                    644 ATTATACAGAAATCCGACAGTACTGCAATCACTGGCGAAATTTTGCTGACATTGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 69, Application US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM SE.
APPLICANT: POULSEN, TIM SE.
APPLICANT: POULSEN, TIM SEN
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR PILING DATE: 2004-05-04
                                                       Gaps
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Length 146656;
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Score 32.8; DB 7; Length 1. Pred. No. 37; 0; Mismatches 42; Indels
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                                                                                                                                                                                                                                                 134099 CTTCCTTATATTAATCACTTATCCTTAAATAGAATTTATT 134138
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US-11-112-908-23/C

Sequence 23, Application US/11112908

Publication No. US205502605591

GENERAL INFORMATION:
APPLICANT: Harris, Cole
APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REFERENCE: 04-164-US
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT FILING DATE: 2005-04-22
PRIOR PRILING DATE: 2004-04-23
PRIOR PRILING DATE: 2004-04-23
PRIOR PELLORION NUMBER: US 60/55,978
PRIOR FILING DATE: 2004-06-01
PRIOR FILING DATE: 2004-10-30
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-30

PRIOR FILING DATE: 2004-11-07

PRIOR FILING DATE: 2004-11-07

PRIOR FILING DATE: 2004-12-07

NUMBER OF SEQ ID NOS: 511

SEQ ID NO 23
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Pred. No. 43
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     Query Match 2.6%;
Best Local Similarity 58.0%;
Matches 58; Conservative (
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SOFTWARE: Patentin version 3.3
SEQ ID NO 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-23
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Matches 55; Conserva
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DB 6;

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Best Local Similarity
Matches 82; Conserv
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US-10-750-185-29504
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Matches 104;
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                       Query Match
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Publication No. US20050272054A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995, 561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                          644 ATTATACAGAAATCCGACAGTACTGCAATCACTGGCGAAATTTTGCTGACATTGATGATT
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                                                                                    Gaps
                                      Length 190882;
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; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: NMI GENOMICS, INC.
; APPLICANT: NMI GENOMICS, INC.
; APPLICANT: ROERPELD, Bavid
; APPLICANT: ROERPELD, David
; APPLICANT: ROERPELD, David
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TILLE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 53897
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                                                                                 Indels
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                                                                                                                                                                                                          704 CCTGGAAAAGTATAAAGAGTATCTTGGACTGGACATCTTT
                                           DB 7;
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                                      Query Match 2.6%; Score 32.8; D
Best Local Similarity 58.0%; Pred. No. 44;
Matches 58; Conservative 0; Mismatches
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US-10-750-185-53897
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ORGANISM: Homo sapiens
US-10-995-561-13246
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LENGTH: 86081
US-11-121-086-69
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; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
                                                                                                                         104 GATTGGCAAGGACGCCTACCATGGCTGGCTGCACTGGGAGCGCTTCATGTGCAACCTTG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        500 GACACATTTAGTGAATAACAATGATGCAGAAAAGCCATAATACATTTTGGAGAGAGT 559
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                                                                                                                                                                                                                                    164 ACTGCCAGGAAGAGCCAGATTCCTGCATCAGTGAGAAAGCTCTTCATGGAGATGGCAGAGC 223
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           Length 86081;
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Pred. No. 2.5;
0; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MAIL100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR PLILING DATE: 2002-12-31
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2.5%; Scor.
48.0%; Pred. No. 41,
... 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 29504, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: PMI GENONICS, INC.
APPLICANT: KERR, Richard
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: BAFES, Stephen
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SOFTWARE: Patentin version 3.1
SEQ ID NO 29504
LENGTH: 1254
                                                                      82; Conservative
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completed: December 26, 2005, 10:57:02
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Job time :
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                                                                                                                                                                                                                                                                                                                                                                                                                     164 ACTGCCAGGAAGAGCCAGATTCCTGCATCAGTGAGAAGCTCTTCATGGAGATGGCAGAGC 223
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Sequence 60280, Application US/10750185

Publication No. US200526603A1

GENERAL INFORMATION:

APPLICANT: PMI GENOMICS, INC.

APPLICANT: ROSENFELD, David

APPLICANT: ROSENFELD, David

APPLICANT: BATES, Stephen

APPLICANT: BATES, Stephen

APPLICANT: PAPLICANT: POLMIS

TITLE OF INVENTIN, Dennis

TITLE OF INVENTINON: COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MMI1100-2

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT FILING DATE: 2003-12-31

PRIOR PRIING DATE: 2003-12-31

NUMBER OF SEQ ID NOS: 64922

SOFTWARE: PALENTIN VERSION 3.1

SEM DID NOS: 64922

SOFTWARE: PALENTIN VERSION 3.1
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                                                                                                                                                                                                                                                                                DB 6; Length 201;
                                                                                                                                                                                                                                                                                                                           87; Indels
TITLE OF INVENTION: DETECTION AND USES THEREOF PILE REFERENCE: CLOOD.559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE PARESEQ for Windows Version 4.0
LENGTH: 201
                                                                                                                                                                                                                                                                                Score 31.8; DB
Pred. No. 0.83;
0; Mismatches
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; ORGANISM: Bovine 19866880544951
US-10-750-185-60280
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                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 84; Conserv
                                                                                                                                                                                                                                US-10-995-561-29100
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US-10-750-185-60280
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1462 CAGTCATGAGGCCATTGGTCTCCTTCCAGAGCACCACGTCATAAACCAGTATTTAAATCCC 1403
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                                                                                         APPLICANT: Zuker, Charles S.
APPLICANT: Erlenbach, Isolda
APPLICANT: Broon, Mark A.
APPLICANT: Ryba, Nicholas J. P.
APPLICANT: Ryba, Nicholas J. P.
APPLICANT: The Regents of the University of California
APPLICANT: The Government of the United States of America
APPLICANT: The Government of the United States of America
APPLICANT: Department of Health and Human Services
APPLICANT: Department of Health and Human Services
APPLICANT: Compled Receptor
TITLE OF INVENTION: A Mammalian Magnesium/Manganese Sensing G Protein
TITLE OF INVENTION: Coupled Receptor
FILE REFERENCE: 02307E-145400US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: mouse magnesium/manganese sensing G protein OTHER INFORMATION: coupled receptor (GPCR) R5.24, Mg receptor, Mn OTHER INFORMATION: receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/841,129
CURRENT FILING DATE: 2004-05-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VEY: 2.1
Sequence 3, Application US/10841129
Publication No. US20050250113A1
GENERAL INFORMATION:
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd. Copyright

- protein search, using sw model OM protein December 24, 2005, 08:33:27 Run on:

; Search time 187 Seconds (without alignments) 989.190 Million cell updates/sec

Title: Perfect score:

US-10-602-219-12 2314 1 MQLRNPELHLGCALALRFLA......RLRSHINPTGTVLLQLENTM 421 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2443163 segs, 439378781 residues Searched:

Total number of hits satisfying chosen parameters:

2443163

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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1. geneseqp1980s:*

2. geneseqp2000s:*

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8. geneseqp2003s:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AEA27471 AEB43188 ABM79001 AAE28209 ADD84749	ADJ88275 ADM48679 ADU66914 AEA27443	ADD84745 ADJ88271 ADM48675 ADU66910 AEA27439	AAX48575 AAR07305 AAE28208 ADD84747 ADJ88273 ADM48677
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ALIGNMENTS

RESULT 1

AAE28210 standard; protein; 421 AA. (first entry) Human rGAL-8 protein. 27-DEC-2002 AAE28210; AAE28210

Human; alpha-galactosidase; lysosomal enzyme; lysosomal storage disease; therapeutic; rGAL-8.

Homo sapiens.

401. .402 /note= "CTPP cleavage site" Location/Qualifiers US2002088024-A1. Key Cleavage-site

13-NOV-2001; 2001US-00993059. 04-JUL-2002

(GARG/) GARGER S J. (TURP/) TURPEN T H. (KUMA/) KUMAGAI M H.

26-JUL-2000; 2000US-00626127.

Kumagai MH; Garger SJ, Turpen TH,

WPI; 2002-681656/73. N-PSDB; AAD45223. Novel human alpha-galactosidase polypeptide useful for treating lysosomal storage diseases

Claim 7; Page 44; 88pp; English.

The invention relates to human alpha-galactosidase truncated at the carboxy terminus and the production of enzymatically active recombinant human and animal lysosomal enzymes. The invention is useful for producing lysosomal enzymes for tracting lysosomal storage diseases, producing altered or mutated proteins, enzymatically active or otherwise, to serve as precursors or substrates for further in vivo or in vitro processing to

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The invention relates to human alpha-galactosidase derivatives and the nucleic acids encoding them. The polypeptides are used in a method for producing active recombinant human and animal lysosomal enzymes in a plant expression system. The enzymes can be used in enzyme replacement therapy for the therapeutic treatment of human and animal lysosomal diseases. This sequence represents a human alpha-galactosidase derivative polypeptide of the invention.
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Fabry's disease; Gaucher's disease; human; enzyme.
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                                                                                                                                                                                                                                                                                                  100.0%; Score 2314; DB 7;
100.0%; Pred. No. 1.8e-221;
iive 0; Mismatches 0;
                                                                               New polynucleotide for producing active lysosomal enzymes in a plant expression
                                                                                                                                      Claim 7; SEQ ID NO 12; 77pp; English.
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              Kumagai MH
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Best Local Similarity 100.
Matches 421; Conservative
              Turpen TH,
                                                                                                              replacement therapy.
                                         WPI; 2003-801257/75.
N-PSDB; ADD84750.
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produce more effective therapeutic enzyme, for producing antibodies against lysosomal enzymes for medical diagnostic use, and in any commercial process that involves substrate hydrolysis. The present sequence is human rGAL-8 protein
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                                                                                                                         Length 421;
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                                                                                                                        Score 2314; DB 5;
Pred. No. 1.8e-221;
0; Mismatches 0;
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13-NOV-2001; 2001US-00993059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New alpha-galactosidase polypeptides, useful in producing recombinant lysosomal enzymes for the treatment of lysosomal storage diseases, such as Gaucher's disease, Niemann-Pick disease, Fabry disease and Tay-Sachs
                                                                                                                                                                                                                                                                                                                               Galactosidase; Gal; lysosomal enzyme; enzyme replacement therapy;
lysosomal storage disease; Gaucher's disease; Niemann-Pick disease;
Fabry disease; Tay-Sachs disease; cardiovascular; nephrotrophic; human;
                                            Grill LK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pogue GP, Erwin RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 12; 72pp; English.
                                                                                                                                                                                                                  ADM48681 standard; protein; 421 AA.
                                                                                                                                                                                                                                                                                                     Human wild type rGAL-8 protein.
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88US-00160771.
89US-0030081.
92US-00923692.
92US-0093733.
93US-00176414.
94US-00176413.
94US-00136237.
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                                                                                                                                                                                                                                                                           (first entry)
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POGUE G P.
ERWIN R L.
GRILL L K.
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                                                                                                            M 421
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29-DEC-1993;
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14-OCT-1994;
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(POGU/)
(ERWI/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to nucleotide encoding galactosidase (GAL). The invention is useful in gene therapy. The polynucleotides and polypeptides are useful in treating human and animal lysosomal storage diseases, e.g. Pabry's disease and Gaucher's diseases. The present sequence is human GAL protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 RHISPQAKALLQDKDVIAINQDPLGKQGYQLRQGDNFEVWERPLSGLAWAVAMINRQEIG 360
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Pred. No. 1.8e-221
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grill LK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; SEQ ID NO 12; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Erwin RL,
                                                                                                          88US-00160771.

88US-00219279.

89US-00347637.

89US-00363138.

90US-00600244.

91US-00737899.

91US-00737899.

91US-00737899.

91US-00737899.

91US-00737899.

91US-0073743.

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91US-0097733.

92US-0099743.

93US-00997444.

94US-00176444.
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                                                                  2003US-00602219
                                                                                               88US-00160766
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Matches 421; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New lysosomal enzymes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   storage diseases, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Turpen TH, Pogue GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-108227/11.
                                                                                                                                                                                                                                                                                                                                                                              (TURP/) TURPEN T H.
(POGU/) POGUE G P.
(ERWI/) ERWIN R L.
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ERWIN R L.
GRILL L K.
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         US2004016021-A1.
                                                                  23-JUN-2003;
                                                                                                                                                       05-MAY-1989;
08-JUN-1989;
22-OCT-1990;
                                                                                                                                                                                                                  26-JUL-1991;
01-AUG-1991;
31-JUL-1992;
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29-DEC-1993
                                      22-JAN-2004
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Similarity
N-PSDB; ADU66915
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                                                                                                                                                                  ADGYKHMSLALNRTGRSIVYSCEWPLYMWPFQKPNYTEIRQYCNHWRNFADIDDSWKSIK
                                                                                                                                                                             ADGYRHMSLALNRTGRSIVYSCEWPLYMWPFQKPNYTEIRQYCNHWRNFADIDDSWKSIK
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                                                                  1 MOLRNPELHLGCALALRFLALVSWDIPGARALDNGLARTPTMGWLHWERFMCNLDCQEEP
                                                                                                  DSCISEKLFMEMAELMVSEGWKDAGYEYLCIDDCWMAPQRDSEGRLQADPQRFPHGIRQL
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                                 Length 421;
                                                Indels
                               100.0%; Score 2314; DB 8;
llarity 100.0%; Pred. No. 1.8e-221;
Conservative 0; Mismatches 0;
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13-NOV-2001; 2001US-00993059.
20-MAR-2002; 2002US-00103327.
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                               Query Match
Best Local Similarity
                Sequence 421 AA;
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                                                                                                                                                                                                            The present invention relates to the production of human and animal lysosomal enzymes in plants by a transient plant expression system. The invention relates to glucocerebrosidase (GCB, GCR) and alpha-galactosidase enzymes having a post-translational modification provided by the plant expression system. The invention is useful in enzyme replacement therapy for treating lysosomal storage diseases such as Gaucher's disease, Niemann-Pick disease, Pabry's disease and Tay-Sachs disease, Hurler's syndrome and Hurler-Scheie syndrome. The invention is also useful in researches for developing new approaches to medical treatment of lysosomal storage diseases and in industrial processes involving enzymatic substrate hydrolysis. The present sequence is the human alpha-galactosidase protein.
pharmaceutical composition comprising a lysosomal enzyme, useful for nzyme replacement therapy for the treatment of lysosomal storage
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                                                                                                                                                   Disclosure; SEQ ID NO 12; 88pp; English,
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                                                                           diseases, such as Fabry's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEA27445 standard; protein; 421
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Matches 421; Conservative
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The present invention relates to the production of human and animal lysosomal enzymes in plants by a transient plant expression system. The invention relates to glucocarebrosidase (GCB, GCR) and alpha-galactosidase (Gal) enzymes having a post-translational modification provided by the plant expression system. The invention is useful in enzyme replacement therapy for treating lysosomal storage diseases such as Gaucher's disease, Niemann-lick disease, Fabry's disease, Tay-Sachs disease, Hurler's syndrome and Hurler-Scheie syndrome. The invention is also useful in researches for developing new approaches to medical treatment of lysosomal storage diseases and in industrial processes involving enzymatic substrate hydrolysis. The present sequence is the human alpha-galactosidase protein. Note: The present sequence is the SEQ ID NO: 8 which is shown in page 36-38 of the specification. This sequence
361 GPRSYTIAVASLGKGVACNPACFITQLLPVKRKLGFYEWTSRLRSHINPTGTVLLQLENT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polypeptides useful for producing lysosomal enzymes in plants to be utilized in enzyme replacement therapy or for the therapeutic treatment of human or animal lysosomal storage diseases, e.g.
                                                                                                                                                                                                                                                                                                                                                                                   Gauchers disease; metabolic; neurological disease; niemann pick disease; genetic disorder; Fabry disease; metabolic disorder; tay sachs disease; antilipemic; cns-gen.; lysosome storage disease; alpha-galactosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MOLRNPELHIGGALALRFIALVSWDIPGARALDNGLARTPTWGWLHWERFMCNLDCQEEP
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                                                                                                                                                                                                                                                                                                                                           Human alpha-galactosidase protein, rGAL-4, SEQ ID NO: 8 #2.
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100.0%; Pred. No. 1.8e-221;
iive 0; Mismatches 0;
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                                                                                                                                                                                                        AEA27472 standard; protein; 425 AA.
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13-NOV-2001; 2001US-00993059.
20-MAR-2002; 2002US-00103327.
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                                                                                                                                                                                                                                                                                                  11-AUG-2005 (first entry)
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                                             421 M 421
                                                                                        M 421
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                                                                                                                                                                                                                                                       AEA27472;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RHISPQAKALLQDKDVIAINQDPLGKQGYQLRQGDNFEVWERPLSGLAWAVAMINRQEIG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lysosonal enzymes in plants by a transient plant expression system. The invention relates to glucocerebrosidase (GCB, GCR) and alpha-galactosidase (Gal) enzymes having a post-translational modification provided by the plant expression system. The invention is useful in enzyme replacement therapy for traating lysosomal storage diseases such as Gaucher's disease, party's disease, Tay-Sachs disease, Hurler's syndrome and Hurler-Scheie syndrome. The invention is also useful in researches for developing new approaches to medical treatment of lysosomal storage diseases and in industrial processes involving enzymatic substrate hydrolysis. The present sequence is the human alpha-galactosidase protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polypeptides useful for producing lysosomal enzymes in plants to be utilized in enzyme replacement therapy or for the therapeutic treatment of human or animal lysosomal storage diseases,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 28; SEQ ID NO 12; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                     Kumagai MH;
                                                                                                                                                                                                                                                                                                                        (LARG-) LARGE SCALE BIOLOGY CORP.
                                                                                                                                                                                                                             26-JUL-2000; 2000US-00626127.
13-NOV-2001; 2001US-00993059.
20-MAR-2002; 2002US-00103327.
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Les 421; Conservative
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N-PSDB; AEA27444.
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                                                                                          US2005125859-A1.
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                                                  Homo sapiens.
                                                                                                                                       09-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                     Garger SJ,
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lysosomal enzymes for treating lysosomal storage diseases, producing an attered or mutated proteins, enzymatically active or otherwise, to serve as precursors or substrates for further in vivo or in vitro processing to a specialised industrial form for research or therapeutic uses, to produce more effective therapeutic enzyme, for producing antibodies against lysosomal enzymes for medical disgnostic use, and in any sequence is human rGAL-8R protein
The invention is useful for producing
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                                                                                                                                                                                                                                               Query Match
100.0%; Score 2314; DB 5;
Best Local Similarity 100.0%; Pred. No. 1.8e-221;
Matches 421; Conservative 0; Mismatches 0;
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13-NOV-2001; 2001US-00993059
  and animal lysosomal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; alpha-galactosidase; lysosomal enzyme; lysosomal storage disease;
therapeutic; rGAL-8R.
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                                                                                                                               ANYVHSKGLKLGIYADVGNKTCAGFPGSFGYYDIDAQTFADWGVDLLKFDGCYCDSLENL
                                                                                                                                                                                                           ADGYKHMSLALNRTGRSIVYSCEWPLYMWPFQKPNYTEIRQYCNHWRNFADIDDSWKSIK
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                     DSCISEKLFMEMAELMVSEGWKDAGYEYLCIDDCWMAPQRDSEGRLQADPQRFPHGIRQL
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N-PSDB; AAD45224.
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(TURP/) TURPEN T H.
(KUMA/) KUMAGAI M H.
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Fabry's disease; Gaucher's disease; human; enzyme.
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                                                                                                             88US-00160766.

88US-0010771.

88US-00310811.

89US-00347637.

89US-00363138.

90US-0061617.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 427 AA;
                                            US2004016021-A1
                                                                                         23-JUN-2003;
                                                                                                                                                                    -JUN-1989;
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26-JUL-1991
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14-OCT-1994
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                                                                                                                                                                  The invention relates to human alpha-galactosidase derivatives and the nucleic acids encoding them. The polypeptides are used in a method for producing active recombinant human and animal lysosomal enzymes in a plant expression system. The enzymes can be used in enzyme replacement therapy for the therapeutic treatment of human and animal lysosomal diseases. This sequence represents a human alpha-galactosidase derivative polypeptide of the invention.
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                                                                                                  New polynucleotide for producing active recombinant human and animal lysosomal enzymes in a plant expression system that can be used in enzyme
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                                                                                                                                                                                                                                                                                    Length 427;
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                                                                                                                                                                                                                                                                                  100.0%; Score 2314; DB 7;
100.0%; Pred. No. 1.8e-221
tive 0; Mismatches 0;
                                                                                                                                                Claim 7; SEQ ID NO 14; 77pp; English
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                                             Kumagai MH
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Best Local Similarity 100.
Matches 421; Conservative
                                            Garger SJ, Turpen TH,
 GARGER S J.
TURPEN T H.
KUMAGAI M H.
                                                                   WPI; 2003-801257/75
                                                                                                                           replacement therapy.
                                                                              N-PSDB; ADD84752
                                                                                                                                                                                                                                                              Sequence 427 AA;
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The invention relates to nucleotide encoding galactosidase (GAL). The invention is useful in gene therapy. The polynucleotides and polypeptides are useful in treating human and animal lysosomal storage diseases, e.g. Pabry's disease and Gaucher's diseases. The present sequence is human GAL protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANYVHSKGLKLGIYADVGNKTCAGFPGSFGYYDIDAQTFADWGVDLLKFDGCYCDSLENL 180
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                                                                                                                                     New lysosomal enzymes, useful in treating human and animal lysosomal storage diseases, e.g. Fabry's disease and Gaucher's diseases.
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Pred. No. 1.8e-221;
0; Mismatches 0;
Grill LK;
                                                                                                                                                                                                                             Claim 7; SEQ ID NO 14; 71pp; English.
Erwin RL,
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Lysosomal enzyme; glucocerebrosidase; GCB; GCR; alpha-galactosidase; enzyme replacement therapy; lysosomal storage disease; Gaucher's disease; Niemann-Pick disease; Pabry's disease; Tay-Sachs disease; Hurler's syndrome; Hurler's syndrome; Hurler's syndrome; Hurler's syndrome; Hurler-Scheie syndrome; nephrotropic; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                           enzymes for enzyme replacement therapy for treating human and animal lysosomal storage diseases such as Gaucher's disease, Niemann-Pick disease, Pabry disease and Tay-Sachs disease. The present sequence is human wild type rGAL-8R protein. This sequence comprises a human rGAL-8 protein and a ER retention signal. This sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                      ANYVISKGEKLGIYADVGNKTCAGFPGSFGYYDIDAQTFADWGVDLLKFDGCYCDSLENL
                                                                                                                                                                                                                                                                                               121 ANYVHSKGLKLGIYADVGNKTCAGFPGSFGYYDIDAQTFADWGVDLLKFDGCYCDSLENL
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                                                                                                                    100.0%; Score 2314; DB 8; Length 427; 100.0%; Pred. No. 1.8e-221;
                                                                                                                                             Indels
                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human alpha-galactosidase protein #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADU66918 standard; protein; 427
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13-NOV-2001; 2001US-00993059.
20-MAR-2002; 2002US-00103327.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                 Best Local Similarity 100.
Matches 421; Conservative
                                                                                            Sequence 427 AA;
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                                                                                                                     Query Match
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ADU66918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention relates to novel galactosidase (Gal) proteins such rGAL-12, rGAL-12R, r-GAL-25 or rGAL-25R. The methods and compositions the present invention are useful for producing recombinant lysosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New alpha-galactosidase polypeptides, useful in producing recombinant lysosomal enzymes for the treatment of lysosomal storage diseases, such as Gaucher's disease, Niemann-Pick disease, Fabry disease and Tay-Sachs
                                                                                                                                                                                                                                                                                                                                    Galactosidase, Gal, lysosomal enzyme; enzyme replacement therapy;
lysosomal storage disease; Gaucher's disease; Niemann-Pick disease;
Fabry disease; Tay-Sachs disease; cardiovascular; nephrotrophic; human;
  RHISPQAKALLQDKDVIAINQDPLGKQGYQLRQGDNFEVWERPLSGLAWAVAMINRQEIG
                                                       GPRSYTIAVASLGKGVACNPACFITQLLPVKRKLGFYEWTSRLRSHINPTGTVLLQLENT
                                                                                                        Grill LK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Erwin RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, SEQ ID NO 14, 72pp, English.
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                                                                                                                                                                                                                                   ADM48683 standard; protein; 427
                                                                                                                                                                                                                                                                                                             Human wild type rGAL-8R protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88US-00160766.
88US-0016071.
89US-0010081.
90US-00600244.
92US-0099733.
92US-00176414.
94US-00184237.
94US-00184237.
94US-00184237.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAY-1999; 99US-00316572.
26-JUL-2000; 2000US-00626127.
13-NOV-2001; 2001US-00993059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2003US-00602220
                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KUMAGAI M H.
POGUE G P.
ERWIN R L.
GRILL L K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-142650/14.
N-PSDB; ADM48682.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TURPEN T H.
                                                                                                                                                                                                                                                                                                                                                                                                                             US2004023281-A1.
                                                                                                                                             M 421
                                                                                                                                                                      M 421
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-DEC-1992;
29-DEC-1993;
19-JAN-1994;
14-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-FEB-1989;
22-OCT-1990;
31-JUL-1992;
                                                                                                                                                                                                                                                                                    03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-FEB-2004
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(POGU/)
(ERWI/)
(GRIL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TURP/)
                                                                                                                                                                                                           RESULT 11
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us-10-602-219-12.rag

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d polypeptides useful for producing lysosomal enzymes in e utilized in enzyme replacement therapy or for the treatment of human or animal lysosomal storage diseases, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSCISEKLFMEMAELMVSEGWKDAGYEYLCIDDCWMAPQRDSEGRLGADPQRFPHGIRQL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 ANYVHSKGLKLGIYADVGNKTCAGFPGSFGYYDIDAQTFADWGVDLLKFDGCYCDSLENL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 ADGYKHMSLALNRTGRSIVYSCEMPLYMWPFQKPNYTEIRQYCNHWRNFADIDDSWKSIK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SILDWTSFNQERIVDVAGPGGRNDPDMLVIGNFGLSWNQQVTQMALWAIMAAPLFWSNDL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RHISPQAKALLQDKDVIAINQDPLGKQGYQLRQGDNFEVWERPLSGLAWAVAMINRQEIG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to the production of human and animal lysosomal enzymes in plants by a transient plant expression system. The invention relates to glucocerebrosidase (GCB, GCR) and alpha-galactosidase (Gal) enzymes having a post-translational modification provided by the plant expression system. The invention is useful in enzyme replacement therapy for treating lysosomal storage diseases such as Gaucher's disease, Niemann-Pick disease, Fabry's disease, Tay-Sachs disease, Hurler's syndrome and Hurler-Scheie syndrome. The invention is treatment of lysosomal storage diseases and in industrial processes involving enzymatic substrate hydrolysis. The present sequence is the human alpha-galactosidase protein.
                                      Gauchers disease; metabolic; neurological disease; niemann pick disease genetic disorder; Fabry disease; metabolic disorder; tay sachs disease; antilipemic; cns-gen.; lysosome storage disease; alpha-galactosídase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MOLRNPELHLGCALALRFLALVSWDIPGARALDNGLARTPTMGWLHWERFMCNLDCQEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MQLRNPELHLGCALALRFLALVSWDIPGARALDNGLARTPTMGWLHWERFMCNLDCQEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SILDWISFNOERIVDVAGPGGWNDPDMLVIGNFGLSWNQQVTQMALWAIMAAPLFMSNDL
  Human alpha-galactosidase protein, rGAL-8R, SEQ ID NO: 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 2314; DB 9; 100.0%; Pred. No. 1.8e-221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 14; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Kumagai MH;
                                                                                                                                                                                                                                                                                                                                                                                              (LARG-) LARGE SCALE BIOLOGY CORP.
                                                                                                                                                                                                                                                                                                                             13-NOV-2001; 2001US-00993059.
20-MAR-2002; 2002US-00103327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Turpen TH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaucher's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AEA27446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 427 AA;
                                                                                                                                                                                  US2005125859-A1
                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated
plants to be
                                                                                                                                                                                                                                                                                                            26-JUL-2000;
                                                                                                                                                                                                                             09-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                       Garger SJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                  lysosonal enzymes in plants by a transient plant expression system. The invention relates to glucocerebrosidase (GCB, GCR) and alpha-
glaatcosidase enzymes having a post-translational modification provided by the plant expression system. The invention is useful in enzyme replacement therapy for treating lysosomal storage diseases such as Gaucher's disease, Niemann-Pick disease, Fabry's disease and Tay-Sachs disease, Hurler's syndrome. The invention is also useful in researches for developing new approaches to medical treatment of lysosomal storage diseases and in industrial processes involving enzymatic substrate hydrolysis. The present sequence is the
                                                                                                                                             for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SILDWITSFNQERIVDVAGPGGWNDPDMLVIGNFGLSWNQQVIQMALWAMAMAPLFMSNDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPRSYTIAVASLGKGVACNPACFITQLLPVKRKIGFYEWTSRLRSHINPTGTVILQLENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MOLRNPELHLGCALALRFLALVSWDIPGARALDNGLARTPTMGWLHWERFMCNLDCQEEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANYVHSKGLKLGIYADVGNKTCAGFPGSFGYYDIDAQTFADWGVDLLKFDGCYCDSLENL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADGYKHMSLALNRTGRSIVYSCEWPLYMWPFQKPNYTEIRQYCNHWRNFADIDDSWKSIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RHISPQAKALLQDKDVIAINQDPLGKQGYQLRQGDNFEVWERPLSGLAWAVAMINRQEIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                         A pharmaceutical composition comprising a lysosomal enzyme, useful enzyme replacement therapy for the treatment of lysosomal storage diseases, such as Fabry's disease.
                                                                                                                                                                                                                                                                     present invention relates to the production of human and animal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 2314; DB 8; Length 427; 100.0%; Pred. No. 1.8e-221; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                             Disclosure; SEQ ID NO 14; 88pp; English
                                        Kumagai MH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      427 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human alpha-galactosidase protein
LARGE SCALE BIOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
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                                        Turpen TH,
                                                                               WPI; 2004-821274/81.
N-PSDB; ADU66917.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 427 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M 421
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                                        Garger SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                               ADGYKHMSLALMRTGRSIVYSCEWPLYMWPFQKDNYTEIRQYCHHWRNPADIDDSWKSIK
                                                                                                                                                                                                                                                               GPRSYTIAVASLGKGVACNPACFITQLLPVKRKLGPYEWTSRLRSHINPTGTVLLQLENT
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                                                                                                                                                                                           ADGYKHMSLALNRTGRSIVYSCEWPLYMWPFQKPNYTEIRQYCNHWRNFADIDDSWKSIK
                                                                                                                                                                                                                                                 SILDWISFNQERIVDVAGPGGWNDPDMLVIGNFGLSWNQQVIQMALWAIMAAPLFMSNDL
                            MOLRNPELHLGCALALRFLALVSWDI PGARALDNGLARTPTMGWLHWERFMCNLDCQEEP
                                                                                                                                      ANYVHSKGLKLGIYADVGNKTCAGFPGSFGYYDIDAQTFADWGVDLLKFDGCYCDSLENL
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  Indels
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/note= "N-linked glycosylation"

215. 217

note= "N-linked glycosylation"

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/note= "N-linked glycosylation"
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/note= "N-linked glycosylation"
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                                                                     420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prodn of human alpha-galactosidase A - by culturing cells contg the coding sequence and the beta-galactosidase alpha-2,6-sialyl transferase
Length 429;
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345
/note= "putative N-glycosylation site"
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Pred. No. 1.8e-221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "putative N-glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 102-103; 156pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
236
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                                                                                                                                                                                            AAR53765 standard; protein; 429
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Best Local Similarity
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15-NOV-1994
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RESULT 14

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The amino acid sequence of the human alpha-galactosidase A (hAGA). The gane encodes a protein of 429 amino acids. Methods to overexpress and purify the protein include: (1) placing the 1.45 kb human hAGA gene fragment in a mammalian expression plasmid e.g. AAP91023 and purifying c fragment in a mammalian expression plasmid e.g. AAP91023 and purifying conformatography or (ii) by producing a fusion protein comprising hAGA c tused to easily purified protein sequences e.g. the Staphyloccus protein CC A, with cleavage site for a "housekeeping" gene e.g. collagenase cleavage site, inserted between the two sequences in a mammalian expression plasmid. The fusion protein can be easily purified by affinity colromatography and the galactosidase protein released from the fusion protein can be easily purified by affinity corrematography and the galactosidase protein released from the fusion protein can be used for enzyme replacement therapy in patients with the lysosomal storage disorder, Fabry diseases. The protein can also be used in vitro to modify alpha-D-galacto-glycoconjugates in a variety of processes e.g.
                                                                                                                   Recombinant human alpha-galactosidase A prodn. - using a mammalian host cell expression system to obtain high yields of enzymatically active
Bishop DF;
                                                                                                                                                                                                                    Claim 3; Col 43-46; 60pp; English.
Desnick RJ,
                                              WPI; 1994-340330/42
                                                                     N-PSDB; AAQ77861.
Ioannou YA,
                                                                                                                                                                      enzyme.
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ö 9 1 MOLRNPEIHLGCALALRFLALVSWDIPGARALDNGLARTPTWGWLHWERFMCNLDCQEEP Gaps ö 100.0%; Score 2314; DB 2; Length 429; 100.0%; Pred. No. 1.8e-221; tive 0; Mismatches 0; Indels 0; Query Match
Best Local Similarity 100.
Matches 421; Conservative

Sequence 429 AA;

180 DSCISEKLFMEMAELMVSEGWKDAGYEYLCIDDCWMAPQRDSEGRLQADPQRFPHGIRQL 120 DSCISEKLFMEMAELMVSEGWKDAGYBYLCIDDCWMAPQRDSEGRLQADPQRFPHGIRQL 120 ANYVHSKGLKLGIYADVGNKTCAGFPGSFGYYDIDAQTFADWGVDLLKFDGCYCDSLENL 180 9 1 MQLRNPELHLGCALALRFLALVSWDIPGARALDNGLARTPTWGWLHWERFMCNLDCQEEP ANYVHSKGLKLGIYADVGNKTCAGFPGSFGYYDIDAQTFADWGVDLLKFDGCYCDSLENL 61 61 121 121 ď ઠે ద ઠ 셤 ઠે

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M 421 421 completed: December 24, 2005, 08:54:18 Search completed: Do Job time: 189 secs

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2314
1 MQLRNPELHIGCALALRFLA......RLRSHINPTGTVLLQLENTM 421
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(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES		
Result No.	Score	Query Match	Length	DB	ΩI	Description	
-1	2314	100.0	421	e	US-09-993-059-12	Sequence 12,	Appl
7	2314	100.0	421	4	US-10-103-327-12		
m	2314	100.0	421	4	US-10-602-219-12		
4	2314	100.0	421	4	US-10-602-220-12	Sequence 12,	
Ŋ	2314	100.0	421	Ŋ	US-10-851-388-12		
9	2314	100.0	421	Ŋ	US-10-984-389-12		
7	2314	100.0	427	ო	US-09-993-059-14		-
80	2314	100.0	427	4	US-10-103-327-14		
0	2314	100.0	427	4	US-10-602-219-14		Appl
10	2314	100.0	427	4	US-10-602-220-14	Sequence 14,	
11	2314	100.0	427	Ŋ	US-10-851-388-14		
12	2314	100.0	427	ß	US-10-984-389-14		
13	2314	100.0	429	4	US-10-411-037-68		
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15	2314	100.0	429	4	US-10-410-962-68	Sequence 68,	Appl
16	2314	100.0	429	4	US-10-411-049-68		
17	2314	100.0	429	4	US-10-410-930-68		
18	2314	100.0	429	4	US-10-410-997-68		
19	2314	100.0	429	4	US-10-411-012-68		
20	2314	100.0	429	4	US-10-410-913-68		
21	2314	100.0	429	ß	US-10-370-715B-278		
22	2314	100.0	429	'n	US-10-410-980-68		
23	2314	100.0	429	ហ	US-10-410-897-68		
24	2314	100.0	431	m	US-09-993-059-10		
52	2314	100.0	431	4	US-10-103-327-10	Sequence 10,	
56	2314	100.0	431	4	US-10-602-219-10		
27	2314	100.0	431	4	US-10-602-220-10	Sequence 10,	Appl

Sequence 10, Appl	٠,٩	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli		106	8, 7	Seguence 8, Appli	Sequence 8, Appli	Sequence 8, Appli	œ	Sequence 8, Appli	Sequence 4, Appli	4	4,
US-10-851-388-10	US-10-984-389-10 HS-09-993-059-6	US-10-103-327-6	US-10-602-219-6	US-10-602-220-6	US-10-851-388-6	US-10-984-389-6	US-10-131-410-106	US-09-993-059-8	US-10-103-327-8	US-10-602-219-8	US-10-602-220-8	US-10-851-388-8	US-10-984-389-8	US-09-993-059-4	US-10-103-327-4	US-10-602-219-4
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. 88	6 6	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

ULT 1	
09-993-059-12	
equence 12, Application US/09993059	
ublication No. US20020088024A1	
ENERAL INFORMATION:	
APPLICANT: GARGER, Stephen A.	
APPLICANT: TURPEN, Thomas H.	
APPLICANT: KUMAGAI, Monto H.	
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN	
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION	
FILE REFERENCE: 008010087CPUS06	
CURRENT APPLICATION NUMBER: US/09/993,059	
CURRENT FILING DATE: 2001-11-13	
NUMBER OF SEQ ID NOS: 37	
SOFTWARE: FastSEQ for Windows Version 4.0	
EQ ID NO 12	
LENGTH: 421	
TYPE: PRT	

1 MOLRNPELHLGCALALRFLALVSWDIPGARALDNGLARTPTMGWLHWERFMCNLDCQEEP 60 Gaps ö Query Match 100.0%; Score 2314; DB 3; Length 421; Best Local Similarity 100.0%; Pred. No. 1.7e-221; Matches 421; Conservative 0; Mismatches 0; Indels 0

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; ORGANISM: Homo sapiens US-09-993-059-12

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360	301 RHISPQAKALLQDKDVIAINQDPLGKQGYQLRQGDNFEVWERPLSGLAWAVAMINRQBIG 360	. 301	g
360	301 RHISPQAKALLQDKDVIAINQDPLGKQGYQLRQGDNFEVWERPLSGLAWAVAMINRQEIG 360	301	ò
300	SILDWISFNQERIVDVAGFGGWNDPDMLVIGNFGLSWNQQVIQWALWAIMAAPLFMSNDL	241	qq
300	241 SILDWISFNQERIVDVAGPGGNNDPDMLVIGNFGLSWNQQVIQMALWAIMAAPLFMSNDL	241	ò
240	. ADGYKHMSLALNRTGRSIVYSCEWPLYMWPFQKPNYTEIRQYCNHWRNFADIDDSWKSIK	181	q
240	181 ADGYKHMSLALNRTGRSIVYSCEWPLYMWPFQKPNYTEIRQYCNHWRNFADIDDSWKSIK 240	181	È
180	121 ANYVHSKGLKLGIYADVGNKTCAGFPGSFGYYDIDAQTFADWGVDLLKFDGCYCDSLENL	121	QQ
180	121 ANYVHSKGLKLGIYADVGNKTCAGFPGSFGYYDIDAQTFADWGVDLLKFDGCYCDSLENL	121	ò
120		61	qq
120	DSCISEKLFMEMAELMVSEGWKDAGYEYLCIDDCWMAPQRDSEGRLQADPQRFPHGIRQL	61	ò
9	MOLRNPELHLGCALALRFLALVSWDIPGARALDNGLARTPTMGWLHWERFMCNLDCQEEP	П	g
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361 GPRSYTIAVASLGKGVACNPACFITQLLPVKRKLGFYEWTSRLRSHINPTGTVLLQLENT 420

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                                                                                                                                                              Sequence 12, Application US/10103327
Publication No. US20030106095A1
GENERAL INFORMATION:
APPLICANT: GRAGER, Stephen A.
APPLICANT: TURREN, Thomas H.
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
FILE REFERENCE: 008010087CPUSG,
CURRENT APPLICATION NUMBER: US/10/103,327
CURRENT APPLICATION NUMBER: US/09/993,059
FRIOR FILING DATE: 2002-03-20
FRIOR APPLICATION NUMBER: US/09/993,059
FRIOR FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 421
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US-10-103-327-12
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Sequence 12, Application US/10602219 Publication No. US20040016021A1 GENERAL INFORMATION:

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APPLICANT: ALIGNY: ALGORY P.
APPLICANT: TALGANT: ALGORY P.
APPLICANT: Erwin, Robert L.
APPLICANT: Grill, Laurence K.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN PLANTS BY TRANIENT EXPRESSION
FILE REFERENCE: LSBC-0087-CP09B
CURRENT PAPLICATION NUMBER: US/10/602,219
CURRENT PAPLICATION NUMBER: 09/993,059
PRIOR FILING DATE: 2000-11-13
PRIOR PELION FORTE: 2000-11-13
PRIOR FILING DATE: 1000-07-26
PRIOR FILING DATE: 1994-06-21
PRIOR FILING DATE: 1994-06-21
PRIOR FILING DATE: 1994-10-14
PRIOR FILING DATE: 1994-10-14
PRIOR FILING DATE: 1994-01-19
PRIOR PELICATION NUMBER: 07/997,733
PRIOR PELICATION NUMBER: 07/997,733
PRIOR FILING DATE: 1999-10-22
PRIOR FILING DATE: 1999-10-12
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100.0%; Pred. No. 1.7e-221;
ative 0; Mismatches 0;
Large Scale Biology
Turpen, Thomas H.
Pogue, Gregory P.
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ORGANISM: Homo sapiens
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361 GPRSYTIAVASLGKGVACNPACFITQLLPVKRKLGFYEWTSRLRSHINPTGTVLLQLENT 420
361 GPRSYTIAVASLGKGVACNPACFITQLLPVKRKLGFYEWTSRLRSHINPTGTVLLQLENT 420
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                                                                                                                                                                                                                                                                                                                                                          APPLICANT: GARGER, Stephen A.
APPLICANT: TURPEN, Thomas H.
APPLICANT: TURPEN, Thomas H.
APPLICANT: TURPEN, Thomas H.
APPLICANT: KUMAGII, MONCO H.
TITLE OF INVENTION: PRODUCTION OF LYSOSOWAL ENZYMES IN
TITLE OF INVENTION: PRODUCTION OF LYSOSOWAL ENZYMES IN
TITLE OF INVENTION: PRODUCTION OF LYSOSOWAL ENZYMES IN
FILLE REPERENCE: 008010087CPUS06
CURRENT FILLING DATE: 2004-05-21
PRIOR APPLICATION NUMBER: US/09/993,059
PRIOR APPLICATION NUMBER: US/09/993,059
PRIOR APPLICATION NUMBER: US/09/993,059
PRIOR SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
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US-10-984-389-12
; Sequence 12, Application US/10984389
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; Sequence 12, Application US/10851388
; Publication No. US20040234516A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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                                                             Sequence 12, Application US/1060220
| Publication US 040023201A1 |
| GENERAL INPORMATION: US20040023201A1 |
| GENERAL INPORMATION: US20040023201A1 |
| GENERAL INPORMATION: UTDEN, Thomas H. |
| APPLICANT: Large Scale Biology Corporation |
| APPLICANT: Runagal, Monto H. |
| APPLICANT: Runagal, Monto H. |
| APPLICANT: Evrin, Robert L. |
| APPLICANT: Ervin, Robert L. |
| APPLICANTON NUMBER: 09/10/62,20 |
| PRIOR APPLICATION NUMBER: 09/226,127 |
| PRIOR PLILNG DATE: 1999-62-13 |
| PRIOR PLILNG DATE: 1999-10-19 |
| PRIOR PLILNG DATE: 1999-10-19 |
| PRIOR PLILNG DATE: 1999-10-22 |
| PRIOR PLILNG DATE: 1999-10-32 |
| PRIOR PLILNG DATE: 1999-10-31 |
| PRIOR PLILNG DATE: 1999-10-32 |
| PRIOR PLILNG DATE: 1999-10-33 |
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US-10-602-220-12
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Query Match
Best Local Similarity 100.
Matches 421; Conservative
            TYPE: PRT
CORGANISM: Homo sapiens
US-09-993-059-14
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ORGANISM: Homo sapiens
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LENGTH: 427
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Publication No. US20020088024A1
GENERAL INFORMATION:
APPLICANT: GARGER, Stephen A.
APPLICANT: TURPEN, Thomas H.
APPLICANT: KUMAGER, SOUDOUTON OF LYSOSOMAL ENZYMES IN
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
FILE REFERENCE: 008010087C0USO6
CURRENT APPLICATION NUMBER: US/09/993,059
CURRENT FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
SOFFWARE: FASTESQ for Windows Version 4.0
                           APPLICANT: GRAEEK, Stephen A.
APPLICANT: TUREEK, Thomas H.
APPLICANT: TUREEK, Thomas H.
APPLICANT: TUREEK, Monto H.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
FILE REFERENCE: 008010087CPUSO6;
CURRENT APPLICATION NUMBER: US/10/984,389
CURRENT FILING DATE: 2004-11-08
PRIOR APPLICATION NUMBER: US/09/993,059
PRIOR PILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
SEQ ID NO 12
LENGTH: 421
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Publication No. US20050125859A1
                                                                                                                                                                                                                                                                            TYPE: PRT

ORGANISM: Homo sapiens
US-10-984-389-12
                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                             61 DSCISEKLFWEMAELMVSEGWKDAGYEYLCIDDCWMAPQRDSEGRLQADPQRFPHGIRQL 120
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Length 427;
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Publication No. US20030106095A1

GENERAL INFORMATION:
APPLICANT: TUREN, Themas H.
APPLICANT: TUREN, Thomas H.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
FILE REFERENCE: 008010087CPUSO6
CURRENT FILING DATE: 2001-003-327

PRIOR PILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37

SOFTWARE: FREEEE factor Windows Version 4.0
100.0%; Score 2314; DB 3;
100.0%; Pred. No. 1.8e-221;
rative 0; Mismatches 0;
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US-10-002-2201

1 Sequence 14, Application US/1060220

1 Publication No. US2004002281h.

2 GERERAL INFORMATION:

3 APPLICANT: Large Scale Biology Corporation

APPLICANT: Armeai, Monto H.

APPLICANT: Rumgai, Monto H.

APPLICANT: Rumgai, Monto H.

APPLICANT: Robert L.

TILE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN PLANTS BY TRANIENT EXPRESSION

FILE REFERENCE: LSBC-0008-CEPO18

FRIOR PLILING DATE: 2001-11-2

FRIOR PLILING DATE: 2001-11-2

FRIOR PLILING DATE: 1999-05-21

FRIOR PLILING DATE: 1999-05-21

FRIOR PLILING DATE: 1999-10-14

FRIOR PLILING DATE: 1999-10-14

FRIOR PLILING DATE: 1991-10-14

FRIOR PLILING DATE: 1991-10-14
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                            IndelB
  Pred. No. 1.8e-221;
; Mismatches 0;
  al Similarity 100.0%; P. 421; Conservative 0;
Best Local Similarity
Matches 421; Conserv
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| Sequence 14, Application US/1060219|
| Publication No. US20040016021A1|
| GENERAL INFORMATION|
| APPLICANT: Darge Scale Biology Corporation|
| APPLICANT: Turpen, Thomas H. |
| APPLICANT: Gril, Laurence K. |
| TILIAG OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN PLANTS BY TRANIENT EXPRESSION |
| PILE REPERENCE: LSBC-0087-CP09B |
| CURRENT APPLICATION NUMBER: 03/91062, 219 |
| PRIOR APPLICATION NUMBER: 03/91062, 219 |
| PRIOR APPLICATION NUMBER: 03/9106-23 |
| PRIOR APPLICATION NUMBER: 03/10662, 127 |
| PRIOR PLILING DATE: 1939-105-11 |
| PRIOR PLILING DATE: 1939-105-11 |
| PRIOR PLILING DATE: 1930-10-22 |
| PRIOR PLILING DATE: 1930-10-22 |
| PRIOR PLILING DATE: 1930-10-22 |
| PRIOR PLILING DATE: 1930-10-19 |
| PRIOR PLILING DATE: 1930-10-22 |
| PRIOR APPLICATION NUMBER: 03/600,244 |
| PRIOR APPLICATION NUMBER: 03/600,244 |
| PRIOR APPLICATION NUMBER: 03/10-16 |
| PRIOR PLILING DATE: 1930-10-22 |
| PRIOR APPLICATION NUMBER: 03/600,244 |

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ORGANISM: Homo sapiens
US-10-602-219-14
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                                       DSCISEKLFMEMAELMVSEGWKDAGYEYLCIDDCWMAPQRDSEGRLQADPQRFPHGIRQL
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   MOLRNPELHLGCALALRFLALVSWDI PGARALDNGLARTPTMGWLHWERFMCNLDCQEEP
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APPLICANT: TURPEN, Thomas H.
APPLICANT: TURPEN, Thomas H.
APPLICANT: TURPEN, Thomas H.
TITLE OF INVENTION: PRODUCTION OF LYSOSOWAL ENZYMES IN
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
FILE REPERENCE: 008010087CPUSO6
CURRENT APPLICATION NUMBER: US/10/984,389
CURRENT FILING DATE: 2004-11-08
PRIOR FILING DATE: 2004-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PASTESQ for Windows Version 4.0
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100.0%; Pred. No. 1.8e-221;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 421; Conservative
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                                                                                                                                    Length 427;
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| Publication No. US20040234516A1
| GENERAL INFORMATION:
| APPLICANT: GARGER, Stephen A. |
| APPLICANT: TURPEN, Thomas H. |
| APPLICANT: TURPEN, Thomas H. |
| APPLICANT: TURPEN, TOWAGAI, MONCO H. |
| TITLE OF INVENTION: POLANTS BY TRANSIENT EXPRESSION |
| FILE REFERENCE: 0080100817CPUSO6 |
| CURRENT APPLICATION NUMBER: US/10/851,388 |
| CURRENT FILING DATE: 2004-05-21 |
| PRIOR FILING DATE: 2004-1-13 |
| NUMBER OF SEQ ID NOS: 37 |
| SEQ ID NOS: 37 |
| LENGTH: 427 |
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                                                                                                                                  Score 2314; DB 4;
Pred. No. 1.8e-221;
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                                                                                                             100.0%; Scor.
100.0%; Pred. No. x...
0; Mismatches
; SOFTWARE: Patentin version 3.; SEQ ID NO 14; LENGTH: 427; TYPE: PRT ; ORGANISM: Homo sapiens US-10-602-220-14
                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 421; Conservative
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US-10-851-388-14
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US-10-851-388-14
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Qy 181 ADGYKHMSLALNRTGRSIVYSCEWPLYMWPPQKPNYTEIRQYCNHWRNFADIDDSWKSIK 240 Db 181 ADGYKHMSLALNRTGRSIVYSCEWPLYMWPPQKPNYTEIRQYCNHWRNFADIDDSWKSIK 240 Qy 241 SILDWTSFNQERIVDVAGPGGWNDPDMLVIGNFGLSWNQQYTQMALWAIMAAPLFWSNDL 300 Qy 301 RHISPQAKALLQDKDVIAINQDPLGKQGYQLRQGDNFEVWBRPLSGLAWAVAMINRQEIG 360 Db 301 RHISPQAKALLQDKDVIAINQDPLGKQGYQLRQGDNFEVWBRPLSGLAWAVAMINRQEIG 360 CQy 361 GPRSYTIAVASLGKGVACNPACFITQLLPVKRKLGFYEWTSRLRSHINPTGTVLLQLENT 420 CQy 361 GPRSYTIAVASLGKGVACNPACFITQLLPVKRKLGFYEWTSRLRSHINPTGTVLLQLENT 420 CQy 421 M 421	RESULT 14 US-10-411-026-68 US-10-411-026-68 Sequence 68 Application US/10411026 Publication No. US204006391A1 SERENTI INFORMATION: APPLICANT: News Technologies, Inc. APPLICANT: Sept. David FRIOR PRINK DAPPL: Sept. Sept. Sept. David PRIOR PRINK DAPPL: Sept. Sept. David PRIOR PRINK DAPPL: Sept. Sept. Sept. David PRIOR APPLICANTON NUMBER: US 60/391,777 PRIOR PRINK DAPPL: Sept. Sept. Sept. David PRIOR APPLICANTON NUMBER: US 60/391,777 PRIOR PRINK DAPPL: Sept. Se	US-10-411-026-68
QY 241 SILDWTSFNOERIVDVAGPGGNNDPDMLVIGNFGLSWNQQVTQWALWAIMAABLFMSNDL 300 DD 241 SILDWTSFNOERIVDVAGPGGNNDPDMLVIGNFGLSWNQQVTQWALWAIMAAPLFMSNDL 300 QY 301 RHISPQAKALLQDKDVIAINQDPLGKQGYQLRQGDNFFVWERPLSGLAMAVAMINRQEIG 360 DD 301 RHISPQAKALLQDKDVIAINQDPLGKQGYQLRQGDNFFVWERPLSGLAWAVAMINRQEIG 360 QY 361 GPRSYTIAVASLGKGVACNPACFITQLLPVKRKLGFYEWTSRLRSHINPTGTVLLQLENT 420 DD 361 GPRSYTIAVASLGKGVACNPACFITQLLPVKRKLGFYEWTSRLRSHINPTGTVLLQLENT 420 QY 421 M 421 DD 421 M 421	RESULT 13 US-10-411-037-68 US-10-411-037-68 Sequence 68. Application US/10411037 Sequence 68. Application World Model Application No. US20404043446A1 SEQUENCE MODEL INFORMATION: APPLICANT: Neose Technologies, Inc. APPLICANT: Bayer. Robert APPLICANT: Bayer. US 60/328, 523 FRIOR PLINK DATE: 2001-10-10 FRIOR PLINK DATE: 2002-06-07 FRIOR PLINK DATE: 2002-06-07 FRIOR PLINK DATE: 2002-06-07 FRIOR APPLICATION NUMBER: US 60/396, 594 FRIOR PLINK DATE: 2002-06-16 FRIOR APPLICATION NUMBER: US 60/404, 249 FRIOR PLINK DATE: 2002-06-08 FRIOR APPLICATION NUMBER: US 60/404, 249 FRIOR PLINK DATE: 2002-06-08 FRIOR APPLICATION NUMBER: US 60/404, 249 FRIOR PLINK DATE: 2002-06-08 FRIOR APPLICATION NUMBER: US 60/404, 249 FRIOR PLINK DATE: 2002-06-08 FRIOR APPLICATION NUMBER: US 60/404, 249 FRIOR TILL 409 FRIOR APPLICATION NUMBER: US 60/404, 249 FRIOR TILL 409 FRIOR APPLICATION NUMBER: US 60/404, 249 FRIOR TILL 409 FRIOR APPLICATION NUMBER: US 60/404, 249 FRIOR TILL 409 FRIOR TIL	Query Match 100.04; Score 2314; DB 4; Length 429; Best Local Similarity 100.04; Pred. No. 1.8e-21; Antches 421; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 MQLRNPELHLGCALALRFLALVSWDIPGARALDNGLARFPMGMLHWERFMCNLDCQEEF 60 Db 1 MQLRNPELHLGCALALRFLALVSWDIPGARALDNGLARFPMGMLHWERFMCNLDCQEEF 60 Qy 61 DSCISEKLFMEMAELMVSEGWKDAGYEYLCIDDCWMAPQRDSEGRLQADPQRFPHGIRQL 120 Db 61 DSCISEKLFMEMAELMVSEGWKDAGYEYLCIDDCWMAPQRDSEGRLQADPQRFPHGIRQL 120 CQy 121 ANYVHSKGLKLGIYADVGNKTCAGFPGSFGYYDIDAQTFADMGVDLKFPGGCYCDSLENL 180 Db 121 ANYVHSKGLKLGIYADVGNKTCAGFPGSFGYYDIDAQTFADMGVDLKFPGCYCDSLENL 180 Db 121 ANYVHSKGLKLGIYADVGNKTCAGFPGSFGYYDIDAQTFADMGVDLKFPGCYCDSLENL 180

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Search completed: December 24, 2005, 09:11:10 Job time : 168 secs
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                                                                                                                                                                                                                                                                                                                121 ANYVHSKGLKLGIYADVGNKTCAGFPGSFGYXDIDAQTFADWGVDLLKFDGCYCDSLENL 180
                                               ADGYKHMSLALNRTGRSIVYSCEWPLYMWPFQKPNYTEIRQYCNHWRNFADIDDSWKSIK 240
                                                                                                                                      SILDWTSFNQERIVDVAGPGGWNDPDMLVIGNFGLSWNQQVTQMALWAIMAAPLFMSNDL 300
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APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Bow, Xi
APPLICANT: Bow, Caryn
TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
TITLE OF INVENTION: GLYCOCONJUGATION OF G-CSF
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                                                                      181 ADGYKHMSLALNRTGRSIVYSCEWPLYMWPPQKPNYTEIRQYCNHWRNPADIDDSWKSIK
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CURRENT APPLICATION NUMBER: US/10/410,962
CURRENT FILING DATE: 2003-04-09
PRIOR PILING DATE: 2003-04-69
PRIOR PILING DATE: 2001-10-10
PRIOR PILING DATE: 2001-10-19
PRIOR PILING DATE: 2001-10-19
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-25
PRIOR PILING DATE: 2002-06-25
PRIOR PILING DATE: 2002-06-25
PRIOR PILING DATE: 2002-06-25
PRIOR PILING DATE: 2002-06-17
PRIOR PILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-18
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Publication No. US20040077836A1
GENERAL INFORMATION:
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US-10-410-962-68
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December 24, 2005, 08:50:53 ; Search time 13 Seconds (without alignments) 230.993 Million cell updates/sec
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2314
1 MQLRNPELHLGCALALRFLA......RLRSHINPTGTVLLQLENTM 421
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/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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(c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 3, Appli	ť		Sequence 68, Appl	32	8372	Sequence 36, Appl	Sequence 62, Appl	Sequence 8554, Ap	Sequence 62, Appl	236,	1141	103	450,	65,		Sequence 3254, Ap	Sequence 3022, Ap	14,	~	Sequence 8, Appli	Sequence 21, Appl	29,	Sequence 191, App	Sequence 1314, Ap
ID	US-11-073-626-3	US-11-073-626-1	US-11-074-176-108	US-11-057-058-68	US-10-467-657-32	US-10-467-657-8372	US-11-038-284-36	US-11-057-058-62	US-10-467-657-8554	US-11-129-143-62	US-10-510-386-236	US-10-821-234-1141	US-10-467-962B-103	US-10-131-826A-450	US-11-057-058-65	US-10-652-893-2	US-10-467-657-3254	US-10-793-626-3022	US-11-113-424-14	US-11-055-822-2	US-10-645-441-8	US-10-650-326B-21	US-11-051-568-29	US-10-873-528-191	US-10-793-626-1314
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Score	85	82	81	81	80.5	80.5	80	79.5	79	79	78.5	78	78	77.5	77.5	77	76.5	76.5	9/	75.5	75.5	75	75	75	74.5
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Sequence 684, Appl Sequence 67, Appl Sequence 612, Appl Sequence 55, Appl Sequence 6, Appl Sequence 6, Appl Sequence 18, Appl Sequence 1826, Appl Sequence 1826, Appl Sequence 192, Appl Sequence 198, Appl Sequence 198, Appl Sequence 198, Appl Sequence 198, Appl Sequence 198, Appl Sequence 200, Appl Sequence 200, Appl Sequence 200, Appl Sequence 199, Appl Sequence 202, Appl Sequence 199, Appl Sequence 202, Appl Sequence 190, Appl Sequence 190, Appl Sequence 184, Appl Sequence 184, Appl Sequence 184, Appl Sequence 186, Appl Sequence 186, Appl Sequence 186, Appl Sequence 186, Appl Sequence 186, Appl Sequence 186, Appl		gth 437; Indels 80; Gaps 12;	ELMVSEGWKDAGYEYLCI 91 :: : QVKGWKGLFCT 155	IYADVGNKT 141
US-10-467-657-684 US-11-057-058-67 US-11-0467-657-6612 US-11-057-058-59 US-11-103-037-3 US-11-137-465-65 US-10-30-203-6 US-11-137-465-65 US-10-318-284-38 US-11-038-284-46A-192 US-10-928-446A-194 US-10-928-446A-196 US-10-928-446A-199	ALIGNMENTS 73626 1 ccosyl peptide oxida 5/11/073,626 10/232,655 2001-266665 2001-378151 2002-228727 enum	; Score 85; DB 7; Len; Pred. No. 0.62; 29; Mismatches 71;	LDNGLARTPTMGWLHWERFMCNLDCQEEPDSCISEKLFWEWAELMVSEGWKDAGYEYLCI : : LDAGIGLEKTNVWL	DDGWMAPQRDSEGRLQADPQRFPHGIRQLANYVHSKGLKLGIYADVGNKT
3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0	ion US/ 0502445 A, KEIKC A, NOO NOOVEL 1000805	3.7% Similarity 20.4% 6; Conservative	LDNGLARTPTMGWLHWE : - : LDAGIGLEKTNVWL	DDCWMAPQRDSEGRLQA : : GGWLAAAK
74.5 74.5 74.5 73.7 73.7 73.7 70.5 70.5 70.5 70.5 70.5 70.5 70.5 70	1 073-626- ence 3, ication RAL INFO LICANT: LICANT: LICANT: LICANT: LE REFERE E REFERE RENT FILIN OR OR FILIN OR FILIN OR FILIN OR FILIN OR FILIN OR FILIN OR FILIN O	Match Local Simi es 46;	32 LDN 	92 DDC 156 DGG
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US-11-074-176-108
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LENGTH: 944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 DCWMAPQRDSEGRLQADPQRFPHGIRQLANYVHSKGLKLG------IYADVGNKTC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 AGPPGSFG---YYDIDAQTFADWGVDLLKFDGCYCDSLENLADGYKHMSL----ALNRTG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 IGVETADGTKYYADKVVLAAGAWSPTLVDLEDQCCSK----AWVYAHIQLTPEEAAEYKG 256
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Sequence 108, Application US/11074176

Publication No. US20050250135A1

GENERAL INFORMATION:

APPLICANT: Klaenhammer, Todd R.

APPLICANT: Russell, William M.

APPLICANT: Altermann, Eric

APPLICANT: McAuliffe, Oilvia

APPLICANT: Peril, Andrea Accarate

TITLE OF INVENTION: Nucleic Acid Sequences Encoding

TITLE OF INVENTION: Stress Related Proteins and Uses Therefore

FILE REFERENCE: 5051-694

CURRENT APPLICATION NUMBER: US/11/074,176

CURRENT FILING DATE: 2005-03-07

PRIOR FILING DATE: 2004-03-08

NUMBER OF SEQ ID NOS: 381

SOFTWARE: FRASESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 3.5%; Score 82; DB 7; Length 437; 1 Similarity 19.5%; Pred. No. 1.2; 42; Conservative 31; Mismatches 82; Indels
                                                     Sequence 1, Application US/11073626
Publication No. US20050244926A1
GENERAL INFORMATION:
APPLICANT: KUROSAWA, KEIKO
APPLICANT: HIROKAWA, KOZO
APPLICANT: KAJIYAWA, NAOKI
TITLE OF INVENTION: Novel fructosyl peptide oxidase
FILE REPERENCE: 227590US0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 RSIVYSCEWPLYMWPFQKPNYTEIRQYCNHWRNFA 230
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                                                                                                                                                                                                             FILE KEFERENEE: 24.720USO;
CURRENT PAPELICATION NUMBER: US/11/073,626
CURRENT FILING DATE: 2005-03-08
PRIOR APPLICATION NUMBER: US/10/232,655
PRIOR PILING DATE: 2003-01-10
PRIOR PILING DATE: 2001-01-10
PRIOR FILING DATE: 2001-03-04
PRIOR FILING DATE: 2001-12-12
PRIOR PILING DATE: 2001-05-04
PRIOR PILING DATE: 2001-05-04
PRIOR FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Lactobacillus acidophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Coniochaeta sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 42; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-11-074-176-108
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LENGTH: 310
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56 CQEEPDSCISEKLFMEMAELMVSEGWKDAGYEYLCIDDCWMAPQRDSEGRLQADPQRFPH 115
                                                                                                                                                                                                                                    116 GIRQLANYVHSKGLKLGIYADVGNKTCAGFPGSFGYYDIDAQTFADWGVDLLKFDGCYCD 175
                                                                                                                                                                                                                                                                  176 SLENLADGYKHMSLA-----RQY 222
                                                                                                                                                                                                                                                                                                                                                                                        101 PPEFLPEMYNYIKTGKYDCIGTRRVDRKGEAKFKSFLSDMFYKLVNKISNTEIVSGARDY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 CNHWRNFAD----IDDSWKSIKSILDWTSF-----NQERIVDVAGPGGWNDPDMLVI 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 RAMTROMVDAVLSMPEYNRFSKGIFSMVGFKTKYLDYHNVER---VAGESDWNTWKLFKY 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 -----YVHSKGLKLGIYADVGNKTCAG-----FPGSFGYYDIDAQTFADWGV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      467 VDPHIKVDSGYRVHEELRNLGLYV----KTRDGSDYEGWCWPGSAGYPDFTNPTWRAWWA 522
                                                                                                                                                         10 CYNEEESI---PLFYNAVE-KVMQTILDLDYSYWFVNDGSSDKSLEEMRQLQKNDPEHVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 LMVSEGWKDAGYEYLCIDDCWM-APQRDSEGRLQADPQRFPHG---IRQLAN--
                                                               58;
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APPLICANT: LEBOWICE, JONATHAN
APPLICANT: MAGA, JOHN
TITLE OF INVENTION: ACID ALPHA-GLUCOSIDASE AND FRAGMENTS THEREOF
FILE REFERENCE: SYM-011
CURRENT APPLICATION NUMBER: US/11/057,058
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: US 60/543,812
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PATENTIN Version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49; Indels 38;
   3.5%; Score 81; DB 7; Length 310; 20.9%; Pred. No. 0.98; tive 32; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 3.5%; Score 81; DB 7; Length 944; Best Local Similarity 26.5%; Pred. No. 4.3; Matches 36; Conservative 13; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 32, Application US/10467657; Publication No. US20050260581A1; GENERAL INFORMATION:
APPLICANT: CHIRON Spa
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-11-057-058-68
; Sequence 68, Application US/11057058
; Publication No. US20050244400A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 AMDGIADFSQAPLNIAVW 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271 GNFGLS-WNQQVTQMALW 287
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                                                               Conservative
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US-11-057-058-68
Query Match
Best Local Similarity
Matches 54; Conserv
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RESULT 8
US-11-057-058-62
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-----EFDG-FCDRLCNLIQAEKY------GK 398
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                                                                                                                                                                                                                                                                                                                                                             Query Match
3.5%; Score 80.5; DB 6; Length 414;
Best Local Similarity 19.4%; Pred. No. 1.6;
Matches 37; Conservative 30; Mismatches 79; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8372, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANM Maria Rita
APPLICANT: PONTANM Maria Rita
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
APPLICANT: MASIGNANI Vega
PEPLICANT: WONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
                                                                                        CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
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SOFTWARE: SegWin99, version 1.04
SEQ ID NO 8372
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                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-32
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368 MVNE-IEGWPHA----
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US-10-467-657-8372
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APPLICANT: COCKE, DAVID
APPLICANT: COCKE, DAVID
APPLICANT: DEBET, MARTINE
APPLICANT: GIDLEY, MICHAEL, JOHN
APPLICANT: GIDLEY, MICHAEL, JOHN
APPLICANT: GIDLEY, MICHAEL, JOHN
APPLICANT: SAFFORD, RICHARD
APPLICANT: SAFFORD, RICHARD
APPLICANT: SAFFORD, RICHARD
APPLICANT: WESTCOTT, ROGER, JOHN
TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
FILE REPRESENCE: 054163-5003-US
CURRENT FILING DATE: 2005-01-21
PRIOR FILING DATE: 1096-01-21
PRIOR FILING DATE: 1996-05-03
PRIOR FILING DATE: 1996-04-10
PRIOR FILING DATE: 1996-04-10
PRIOR FILING DATE: 1996-04-10
PRIOR PLICATION NUMBER: GB 9509229.2
PRIOR FILING DATE: 1996-04-10
PRIOR PLING DATE: 1996-04-10
PRIOR APPLICATION NUMBER: GB 9509229.2
PRIOR FILING DATE: 1996-04-10
PRIOR PRIOR APPLICATION NUMBER: GB 9509229.2
PRIOR PRIOR DATE: 1996-04-10
PRIOR APPLICATION NUMBER: GB 9509229.2
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PRIOR APPLICATION NUMBER: GB 9509229.2
PRIOR PRIOR DATE: 1996-04-10
PRIOR APPLICATION NUMBER: GB 9509229.2
PRIOR PRIOR DATE: 1996-04-10
PRIOR APPLICATION NUMBER: GB 9509229.2
PRIOR APPLICATION NUMBER: GB 9509229.2
PRIOR PRIOR DATE: 1996-04-10
PRIOR APPLICATION NUMBER: GB 9509229.2
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137 VGNKTCAGFPGSFGYYDIDAQTFADWGVDLLKFDGCYCDSLENLADGYKHMSLALNRTGR 196
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APPLICANT: MAGA, JOHN
TITLE OF INVENTION: ACID ALPHA-GLUCOSIDASE AND FRAGMENTS THEREOF
FILE REPERENCE: SYM-OIL
CURRENT PILING DATE: 2005-02-10
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: US 60/543,812
PRIOR FILING DATE: 2004-02-10
                                                                  --EFDG-FCDRLCNLIQAEKY-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 ADPORF--PHGIRQLANYVHSKGLKL---GIYADVGNKTCAGF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.5%; Score 80; DB 7
25.6%; Pred. No. 4.8;
tive 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 62, Application US/11057058; Publication No. US20050244400A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    Sequence 36, Application US/11038284 Publication No. US20050246793A1 GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 25.6*
Matches 32; Conservative
                                                                                                                                                                                                   399 KHYFPČSLPLF 409
                                         : |: |:|
368 MVNE-IEGWPHA---
                                                                                                                                    197 SIVYSCEWPLY 207
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; ORGANISM: Lathyrus sp.
US-11-038-284-36
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APPLICANT: BERRY, Alan
APPLICANT: BRETZEL, Werner
APPLICANT: BRETZEL, Werner
APPLICANT: HUMBELIN, Markus
APPLICANT: HUMBELIN, Markus
APPLICANT: MAYER, Anne F.
APPLICANT: WAYER, Anne F.
APPLICANT: YELISERV, Alexei A.
TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
FILE REPERBURE: C38435/121866
CURRENT APPLICATION NUMBER: US/11/129,143
CURRENT FILING DATE: 2005-05-13
NUMBER OF SEO ID NOS: 197
SOFTWARE: Patentin version 3.1
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Publication No. US20050244922A1
GENERAL INFORMATION:
APPLICANT: Andersen, Jens Tonne
APPLICANT: Clausen, Ib Groth
APPLICANT: Olsen, Peter Bjarke
APPLICANT: Jorgensen, Steen Troels
APPLICANT: Masmussen, Michael Dolberg
TITLE OF INVENTION: Improved Bacillus Host Cell
FILE REFERENCE: 10294.204-US
CURRENT PILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 248
SEQ ID NO 236
LENGTH: 622
                                                                                               265 PDMLVIGNFGLSWNQQVTQMALWAIMAAPLF---
198 RELLQKLNQ---KQQCNVYLPWGNEAE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 62, Application US/11129143; Publication No. US20050266518A1; GENERAL INFORMATION:
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275 VGIYTDTDPI-KTGVQV 290
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US-11-129-143-62
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                                                                                                                                                                                                                                                                                    ch 3.4%; Score 79.5; DB 7; Length 1827; 1 Similarity 18.3%; Pred. No. 15; 42; Conservative 29; Mismatches 61; Indels 97,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 AGFPGSFGYYDIDAQTFADWGV-----DLLKFDGCYCD
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CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, Version 1.04
LENGTH: 322
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Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: PISTA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MOSIGNANI Vega
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Matches 78, Conservative
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Best Local Similarity
Matches 42; Conserv
                                        LENGTH: 1827

TYPE: PRT

CRGANISM: Rabbit sp.

US-11-057-058-62
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US-10-467-657-8554
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SEQ ID NO 62
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---KVRAEQIAD----- 230
                                                                                  ----MSNDLRHISPQAKALLQDKDV 316
                                                                                                                                      ------GLPFTIVCAKML--LQAAYLLKHAVGIVGVDTGLLHL---ANAL--EKPV 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 SLENLADGYKHMS--LALNRTGRSIVYSCEWPLYMWPFQKPNYTEIRQYCNHWRNFADID 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 ALERLRDISKELSVPIIVKESGNGI--SMETAKLLYSYGIKNFDTSGQGGTNWIAIEMIR 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 DIRRGNWKAESAKNFLDWGVPTAASIIEVR----YSIPDAFLVGSGGIRSGLDAAKAIAL 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 GADIAGWALPVLKSAIEGKESLEQFFRKIIFELKATWMLTGSKNVEALKRSSIVILGKLK 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79; Indels
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326 EEIVKWMGWEPFKELYDLAVELIRRGHAYVDHQTADEIKEYREKKMNSPWRDRPIEESLK 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 GLKLGIYADVGNKTCAGFPGSFGYYDIDAQTFADWGVDLLKFDGCYCDSLENLADGYKHM 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           422 RIKFAPHPKAGDKWCI-YPS----YD-----YAHCTVDSLENIT----HS 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 IKSILDWTSFN---QERIVDVAGPGGWNDPDMLVIGNFGLSWNQQVTQMALWAIM---- 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Plesch, Gunnar
APPLICANT: Blau, Astrid
APPLICANT: Blau, Astrid
APPLICANT: Basechner, Klaus
APPLICANT: Basechner, Klaus
APPLICANT: Klein, Mathieu
TITLE OF INVENTION: Identification of Herbicidally Active Substances
FILE REFERENCE: 2000 857
CURRENT APPLICATION WUMBER: US/10/467,962B
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: PCT/EP02/01466
PRIOR FILING DATE: 2002-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Juery Match
3.4%; Score 78; DB 6; Length 786;
3est Local Similarity 19.0%; Pred. No. 6.7;
4atches 76; Conservative 39; Mismatches 106; Indels 180;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 NPELHLGCALALRFLALVSWDIPGARALDNGLAR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 TPTMGWLHWERFMCNLDCQEE------
| ::: : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | 
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; Publication No. US20050246784A1
; GENERAL INFORMATION:
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Sequence 450, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
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Gerritsen, Mary E.
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 109
SOFTWARE: Patentin Vers. 2.0
SEQ ID NO 103
LENGTH: 786
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APPLICANT: Bereeini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers Luc
APPLICANT: Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OKGANITONI: ALLONI
US-10-467-962B-103
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APPLICANT:
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Publication No. US20050255114A1

GENERAL INFORMATION:
APPLICANT: Inback, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REPERENCE: 821A
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR PILING DATE: 2003-04-07
NUMBER OF SEO ID NOS: 1704
SOFTWARE: PL SEO Genes Version 1.0
SEQ ID NO 1141
LENGTH: 760
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                                                                                                                                                                                                                                                                                                                                                 151 YYDIDAQTFADWG-----VDLLKFDGCYCDSLEN---LADGY--KHMSLALNRTGRSIV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          285 NYEPARGNVADWGDSYGNRVDRFLAGVAYLDGERPSFVMARGYYTRTVLVAYNFRGGKLT 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 YSCEWPLYMWPFQK--PNYTEIRQYCNHWRNFADIDDSWKSIKSILDWTSFNQERI---- 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----FGLSWNQQVTQMALWA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               386 AVDHDGKGLYSTGWGHGDAMHTGNLDPSRPGLEVFQVHENSNSPYGLSFRDAKTGKIIWG 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      289 I------MAAPLFMSNDLRHISPQAKA---LLQDKDVIAINQDPLGKQGYQLRQGDN 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : | : | : | : | : | | 362 RIVTNYFSAHDNDANLQMDIFLEEDGNVNSKLTKDSVMNYHCWNEAWMTRPDLPVGFGGW 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 ----APQRDSEGRLQADP---QRFFHGIRQLANYVHSKGLKLGIYADVGNKTCAGFPGS 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 APORDSEGRLOADPORFPHGIRQLANYVHSKGLKLGIYADVGNKTCAGFPGSFG-----
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                                                                                                                                                                                                                              Gaps
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                                                                                                                                                 Query Match
3.4%; Score 78.5; DB 6; Length 622;
Best Local Similarity 21.4%; Pred. No. 4.4;
Matches 65; Conservative 24; Mismatches 94; Indels 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84;
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19.2%; Pred. No. 6.4;
tive 25; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               422 QAVDSTPQENSDGMYRCGPASVQAIKHG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254 -VDVAGPG----GWNDPDMLVIGN-----
   ; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-236
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Best Local Similarity 19.23
Matches 40; Conservative
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US-10-821-234-1141
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Godowski, Paul J.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 SEGRLOADPORFPHGIROL-----ANYVH-----SKGLKLGIYADVGN---KTCA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 --GFPGSFGYYDIDAQTFADWGVDLLKFDGCYCDSLENLADGYKHMSLALNRTGRSIVYS 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 C---EWPL-----YMWP--FQKPNYTEIRQYCNHWRNFAD--IDDSWKSIKSIL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 DWTSFNOERIVDVAGPGGWNDPDMLVIGNFGLSWN--QQVTQMALWAIMAAPLFMSN--- 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----TLAGNL----TLAGNL---WDCGRNVCALASW----LSNFQG 334
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                                                                                                                                     APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330412.8
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 RNSFAGLFKLTELHLE-----HNDLVKVNFAHFPRLISL-----HSLCLRRNKVAIVVS
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NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48; Mismatches 107; Indels 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.3%; Score 77.5; DB 6; Length 522; 23.3%; Pred, No. 4.4;
                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR PILING DATE: 1997-06-18
PRIOR PILING DATE: 1997-06-18
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059113
PRIOR PLING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR APPLICATION NUMBER: 60/059184
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-19
PRIOR PLING DATE: 1997-09-19
PRIOR PLING DATE: 1997-09-19
PRIOR PLING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
                                            Stewart, Timothy A
                                                                                           Watanabe, Colin K
Wood, William
Sherwood, Steven
Smith, Victoria
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Best Local Similarity 23.3
Matches 85; Conservative
                                                                     Tumas, Daniel
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GTMAL 435
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390 VVILDPGISTNKT----YETYIRGMKH-D 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   277 WNQQVTQMALWAIMAAPL--FMSNDLRHISPQAKALLQDKDVIAINOD--PLGKQGYQLR 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             469 ISNFISSPPIPGSTLDNPPYKINNSGVMLPIINKTIPPTAMHYGDIPEYNVHNLFGYLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 GIYADVG---NKTCAGFPGSFGYYDIDAQTFADWGVDLLKFDGCYCDSLENLADGYKHMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 207;
                                     GENERAL INFORMATION:
APPLICANT: LEBOWitz, Jonathan
APPLICANT: LEBOWitz, Jonathan
APPLICANT: Maga, John
TITLE OF INVENTION: ADDID ALPHA-GLUCOSIDASE AND FRAGMENTS THEREOF
FILE REFERENCE: SYM-011
CURRENT APPLICATION NUMBER: US,11/057,058
CURRENT FILING DATE: 2005-02-10
PRIOR FILING DATE: 2006-02-10
NUMBER OF SEQ ID NOS: 68
SOFTWARE: Patentin version 3.3
SEQ ID NO 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. Similarity 17.7%; Pred. No. 9.1; Similarity 17.7%; Pred. No. 9.1; S4; Conservative 47; Mismatches 136;
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Sequence 65, Application US/11057058
Publication No. US20050244400A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 ILDWTS------
                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Spinacia oleracea
US-11-057-058-65
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Job time : 14 secs

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56545, A 55673, A 4, Appli 14, Appl

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45064, A 23, Appli 23, Appli 4, Appli 6, Appli 6, Appli 161, Appl 107, Appl 107, Appl 1, Appli 31, Appli 31, Appli 31, Appli 8371, Ap

Sequence Sequence Sequence Sequence

Minimum DB Maximum DB

Searched:

Sequence Sequence Sequence

Sequence Seq Sequence

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Run on:

Sequence:

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RESULT 1
US-11-073-112-5
; Sequence 5, Application US/11073112
; Sequence 5, Application US/11073112
; Publication No. US20050260627A1
; GENERAL INFORMATION:
; APPLICANT: Hintz et al.
; TITLE OF INVENTION: Mannosidases and Methods for using the Same
; FILE REPERENCE: 62447-02
; CURRENT APPLICATION NUMBER: US/11/073,112
; CURRENT FILING DATE: 2005-03-03
; PRIOR APPLICATION NUMBER: US 10/089,211
; PRIOR APPLICATION NUMBER: US 10/089,211
; PRIOR APPLICATION NUMBER: 60/157,341
; PRIOR APPLICATION NUMBER: 60/157,341
; PRIOR FILING DATE: 2000-10-02
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NOS: 25
; SEQ ID NO 5
; SEQ I
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62
32
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18
Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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; ORGANISM: Aspergillus nidulans
US-11-073-112-5
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23.57%
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Best Local Similarity:
Query Match:
DB:
    Alignment Scores:
Pred. No.:
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-MODEL=frame+p21.model -DEV=xlp
-MODEL=frame+p21.model -DEV=xlp
-MODEL=frame+p21.model -DEV=xlp
-G=cgnz 1/USPTO spool p/US10602219/runat_23122005_151144_17285/app_query.fasta_1.583
-DS=Published Applications NA New -OFWT=fastap -SUFFXIx=p2n.rnpbn -MINNATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=b1ts -START=1 -END=-1 -MATRIX=b1osum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pcto -NORM=ext -HBAPSIZE=500 -MINLEN=0
-MAXEN=2000000000 -USER=US10602219 GCGN 1 1 183 @runat 23122005_151144_17285
-NCPU=5 -NOWHCG -DBY TINEOUT=120 -WARN TIMEOUT=30 -THERDS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAROP=6 -FGAPEXT=7 -YGAPOP=10-YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 22, Appl
Sequence 56907, A
Sequence 111, App
Sequence 4, Appli
Sequence 31179, A
Sequence 35182, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 36, Appl
                                                                                                          December 26, 2005, 13:48:48; Search time 282 Seconds (without alignments) 774.752 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                      MQLRNPELHLGCALALRFLA......RLRSHINPTGTVLLQLENTM 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Applications NA New:*

1: /cgn2 6/ptodata/1/pubpna/US06 NEW PUB.seq:*
2: /cgn2 6/ptodata/1/pubpna/US06 NEW PUB.seq:*
3: /cgn2 6/ptodata/1/pubpna/US07 NEW PUB.seq:*
4: /cgn2 6/ptodata/1/pubpna/PCT NEW PUB.seq:*
5: /cgn2 6/ptodata/1/pubpna/US10 NEW PUB.seq:*
6: /cgn2 6/ptodata/1/pubpna/US10 NEW PUB.seq:*
7: /cgn2 6/ptodata/1/pubpna/US11 NEW PUB.seq:*
8: /cgn2 6/ptodata/1/pubpna/US11 NEW PUB.seq:*
9: /cgn2 6/ptodata/1/pubpna/US11 NEW PUB.seq:*
10: /cgn2 6/ptodata/1/pubpna/US11 NEW PUB.seq:*
                GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                               nucleic search, using frame_plus_p2n model
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US-10-933-025-22
US-10-750-185-56907
US-11-117-187-211
US-11-073-112-4
US-10-750-185-3182
US-10-750-185-3182
US-11-112-908-36
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Maximum Match 100%
Listing first 45 summaries
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1766 6 U
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Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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94.5
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                                                                                                                                                                         Title:
Perfect score:
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Database :

Result Š Š

Sequence 3253, Ap Sequence 121, App

13359,

Sequence Sequence Sequence N

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TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                 Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 YCYS-----TYrCYSASpSerLeuGluAsnLeuAla--------- 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----AspGlyTyrLysHisMetSerLeuAlaLeuAsnArgThrGly-- 195
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                                                                                                                                                                         ----GAATGGTGGCGCAGACTCGTA 782
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                                                                                                                                                                                                                                                                            pCysTrpMetAlaProGlnArgAspSerGluGlyArgLeuGlnAlaAspProGlnArgPh 113
                                                                                                                                                                                                                                                                                                          843 CCGCTGGGTCGCAGCTGCCGAGTCGAGCATCAACCATCTGGCTTCGCACCCGTCCACCCG 902
                                                                                                                                                                                                                                                                                                                                         113 eProHisGlyIleArgGlnLeuAlaAsnTyrValHisSerLysGlyLeuLysLeuGlyIl 133
                                                                                                                                                                                                                                                                                                                                                                     903 ccca---cacgrgacrrrcrrgcccacrrac----aacgaggaggarcagcrgcccr 953
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                                                           569 CCCGGAGCCAGCGCAGTA---------CGAACCGTTCCCTGGATTGAT 707
                                                                                                                                                  66 GluLysleuPheMetGluMetAlaGluLeuMetValSerGluGlyTrpLys-AspAlaGl 85
                                                                                         47 TrpGluArgPheMet---CysAsnLeuAspCysGlnGluGluProAspSerCysIleSer 65
                                                                                                                                                                                                                  85 yTyrGluTyrLeu-----CysIleAspAs 93
                            27 ProGlyAlaArgAlaLeuAspAsnGlyLeuAlaArgThrProThrMetGlyTrpLeuHis 46
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Publication No. US20050265987A1
GENERAL INFORMATION:
APPLICANT: ROSEN, STEVEN
APPLICANT: HEMMERICH, STEFAN
APPLICANT: TOMITA, MEGUMI
TILLE OF INVENTION: SUlfotransferases and methods of use
TILLE OF INVENTION: thereof
FILE REFERENCE: UCAL-230CON
CURRENT APPLICATION NUMBER: US/10/933,025
CURRENT FILING DATE: 2004-09-01
PRIOR APPLICATION NUMBER: 10/025,966
PRIOR FILING DATE: 2001-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1230 ATGGCGCGTCACAGGTGATGGAACGTACCTCGAATGG
US-10-602-219-12 (1-421) x US-11-073-112-5 (1-1515)
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US-10-933-025-22/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 SeriysGlyLeuLysLeuGlyIleTyrAlaAspValGlyAsnLysThrCysAlaGlyPhe 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 ProGlySerPheGlyTyr-----TyrAspIleAspAlaGlnThrPheAlaAspTrp 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuGlnAlaAspProGlnArgPheProHisGlyIleArgGlnLeuAlaAsnTyrValHis 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 -----SerTrpAsnGlnGlnValThrGln 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 GlyTyrLysHisMetSerLeuAlaLeuAsnArgThrGlyArgSerIleValTyrSerCys 202
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Matches:
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PRIOR APPLICATION NUMBER: 60/258,577
PRIOR FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 60/267,831
PRIOR FILING DATE: 2001-09-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 268685
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                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc_feature; LCATION: (1)...(268685); OTHER INFORMATION: n = A,T,C or G US-10-933-025-22
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6 ProGluLeuHisLeuGlyCysAlaLeuAlaLeuArgPheLeuAlaLeuValSerTrpAsp	65SerGluLysLeuPheMetGluMetAlaGluLeuMetValSerGluGlyTrpLy 349 GCCTGGGAACGGGTTTTCTGCGCCTTGAGGAA	102 rd1u	532 145 577 165	181 aAspGlyTytLysHisMetSerLeuAlaLeuAsnArgThrGlyArgSerIleValTyrSe 181 JALLINIELE	221 lnTyrCysAsnHisTrpArgAsnPheAlaAsp	261 lyTrpAenAspProAspMetLeuVallleGlyAsnPheGlyLeuSer 774	Oy 294 LeuPheMetSerAsn	Qy 327 GlnGlyTyrGlnLeuArgGlnGlyAspAsnPheGluValTrp-Gl 341
88888	8 8 8	68686	 8 & 8 & 4	3 8 8 8	888		8888	&. — ;
Oy 284 MethlaLeuTrphlaIleMethlaAlaProLeuPheMetSerhsnAspLeuArgHislle 303	341GluàrgProLeuSerGlyLeuàlaTrpàlaValàlaMetileàsnàrgGlnGlu	Qy 366ThrileAlaValAlaSerLeuGlyLy8GlyValAlaCy8 378 Db 57159 GCTTATATCCGGTCGTCTCTGGCTCTGGCAGGTCCTGGTACCCAAGGCTGGGTGCC 57100 Qy 379 AsnProAlaCysPhe	ATCACAGCTACTGCTGATTCACTGCACTGCACTGCACTG	Sequence 56907, Application US/10750185 ; Publication No. US20050260603A1 ; GENERAL INPORMATION: ; APPLICANT: MMI GENOMICS, INC. ; APPLICANT: KERR, Richard ; APPLICANT: ROSENFELD, David ; APPLICANT: ROSENFELD, David ; APPLICANT: HOLM, Tom	LLI PPL LLI NG	; NUMBER OF SEQ ID NOS: 64922 ; SOFTWARE: PatentIN version 3.1 ; SEQ ID NO 56907 ; LENGTH: 1241 ; TYPE: DNA ; ORGANISM: Bovine 19866881771060 US-10-750-185-56907	1.44 Length: 94.00 Matches: y: 30.51% Conserva irity: 20.49% Mismatch irity: 4.06% Indels: 6 Gaps:	US-10-602-219-12 (1-421) X US-10-750-185-56907 (1-1241)

uargProLeuSerGlyLeuAlaTrpalaValalaMet	Db 566170 CAAATGCGGCTGCAACCTCCGCCACGTCATCCCGACGGTCCGATCTCCACGGTTCTCCACGGTTCTCCACGGTTCTCCACGGTTCTCTCACGGTTCTCTCACGGTTCTCTCACGGTTCTCTCGCAAGGTCCTTCTCTCGCAAGTTGTAATTATACAAATTGGTCTTCTCTCGCAGTGTCTCTCTC
361 yProArgSerTyrThrIleAlaValAlaSerLeuGlyLysGlyVa 376	Qy 150 GlyTyrTyrAspileAspAlaGlnThrPheAla
'HULT 4 11-117-187-211 dequence 211, Application US/11117187 dequence 211, Application US/11117187 dequence 211, Application World US/11117187 deput Nov. US20050266560A1 APPLICANT: PREUSS, DAPHNE APPLICANT: COPENHAVER, GREGORY TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS FILE REFERENCE: ARCD:309US CURRENT APPLICATION NUMBER: US/11/117,187 CURRENT APPLICATION NUMBER: US/09/531,120 PRIOR FILING DATE: 2000-03-17 PRIOR FILING DATE: 2000-03-17 PRIOR FILING DATE: 1999-03-18 NUMBER OF SEQ ID NOS: 212 SEGTWARE: PatentIn Ver. 2.1 LENGTH: 1082144 CREATION NO 211 LENGTH: 1082144 ARANIANA ARABIGORBIS thaliana ORGANISM: Arabidopsis thaliana	172 CYSTYLCYSASPSETLEUGIUASNLEUAIAAS
Length: 1082144 Matches: 76 Conservative: 42 Mismatches: 117 Indels: 20 Gaps: 20	Db 566686 TGGCCTCTTGACTACACCAGTAATTTCTTTGATACTACA Qy 261 GlyTrpAsnAspProAspMetLeuVallieGlyAsnPheGlyLeu Db 566725CCTAAAAGCAGTAGAGTGGGGAAGAACAGATTTGTGGAGCAGATCA Qy 276 SerTrpAsnGlnGlnValThrGlnMetAlaLeuTrpAlalleMetAlaAlaProLeuPhe
LeuargasnProGluLeuHisLeuGlyCysAlaLeualaLeuargPheLeualaLeuVal 22 LeuargasnProGluLeuHisLeuGlyCysAlaLeualaLeuargPheLeualaLeuVal 22 :: ::	Oy 296 MetSerAsnAspLeuArgHisIleSerProGlnAlaLysAlaLeuLeuGlnAspLysAsp
LeuAspCysGlnGluGluProAspSer TTTCAAATCGATAACGTTCGGATCAG GluLeuMetValSerGluGlyTrpLys CysTrpMetAlaProGlnArgAspSer CysTrpMetAlaProGlnArgAspSer ProHisGlyAACTCT	RESULT 5 US-11-073-112-4 i Sequence 4, Application US/11073112 publication No. US20050260627A1 general INFORMATION: APPLICANT: Hintz et al. TITLE OF INVENTY Mannosidases and Methods for using the Same; FILE REFERENCE: 6.2447-0.2 CURRENT APPLICATION NUMBER: US/11/073,112 CURRENT PILING DATE: 2005-03-03. PRIOR APPLICATION NUMBER: US 10/089,211 PRIOR FILING DATE: 2002-02-25 PRIOR APPLICATION NUMBER: PCT/US00/27210 PRIOR FILING DATE: 2000-10-02

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eProHisGlyIleArgGlnLeuAlaAsnTyrValHisSerLysGlyLeuLysLeuGlyIl 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 eTyralaAspValGlyAsnLysThrCysAlaGlyPheProGlySerPhe-----GlyTy 151
                                                                                                                                                                                                                                                                                                                                                                                                                            pCysTrpMetAlaProGlnArgAspSerGluGlyArgLeuGlnAlaAspProGlnArgPh 113
                                                                                                                                                                                                                                                                                                                                 GluLysLeuPheMetGluMetAlaGluLeuMetValSerGluGlyTrpLys-AspAlaGl 85
                                                                                                                                                                                                                                    27 ProGlyAlaArgAlaLeuAspAsnGlyLeuAlaArgThrProThrMetGlyTrpLeuHis 46
                                                                                                                                                                                                                                                                                                                                                                                yTyrGluTyrLeu------Cys1leAspAs
                                                                                                                                                                                                                                                                                    47 TrpGluArgPheMet----CysAsnLeuAspCysGlnGluGluProAspSerCysIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 31179, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: HOMI GENOVICS, INC.
APPLICANT: RAIGHARD
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MA11100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US/827,482
                                                                                                                             2177
45
23
49
46
                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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PRIOR APPLICATION NUMBER: 60/157,341
PRIOR FILING DATE: 1999-10-01
                                                                                                                                                                                                                                                 1059 CCCGGAGCCAGCGCAGTA---
                                                                    TYPE: DNA ORGANISM: Aspergillus nidulans
                     NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.3
SEQ ID NO 4
LENGTH: 2177
                                                                                                                             6.48
91.50
41.72%
27.61%
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Best Local Similarity:
Query Match:
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US-10-750-185-31179
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Pred. No.:
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Indels:
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; Sequence 35182, Application US/10750185

; Publication No. US20050260603A1

; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.
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                                                                                                                       ; TYPE: DNA
; ORGANISM: Bovine 19866880843346
US-10-750-185-31179
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PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: Patentin version 3.1
SEQ ID NO 31179
LENGTH: 2716
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21.15%
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 GlnMetAlaLeuTrpAlaIleMetAlaAlaProLeuPheMetSerAsnAspLeuArgHis 302
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199 lTyrSerCys---GluTrpProLeuTyrMetTrpProPheGlnLysProAsnTyrThrGl 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 HisTrpArgAsnPheAlaAspIleAspAspSerTrpLysSerIleLysSerIleLeuAsp 244
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                                                                                                                                                                                                   Sequence 36, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REFERENCE: 04-164-US
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT PILING DATE: 2004-04-22
FRIOR FILING DATE: 2004-04-23
FRIOR FILING DATE: 2004-06-01
; PRIOR FILING DATE: 2004-06-01
; PRIOR PELING DATE: 2004-11-30
; PRIOR RPLICATION NUMBER: US 60/631,702
; PRIOR PELING DATE: 2004-11-30
; PRIOR FILING DATE: 2004-11-30
; PRIOR FILING DATE: 2004-11-30
; NUMBER OF SEQ ID NOS: 511
; SOFFWARE: Patentin version 3.3
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: LOCATION: (49350)..(49350)

: OTHER INFORMATION: n is a, c,

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Best Local Similarity:
Query Match:
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                                                                              APPLICANT: PANES, Dennies TO PERFECTIONS FOR INFERRING BOVINE TRAITS FILE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS FILE REFERENCE: MM11100-2 CURRENT APPLICATION NUMBER: US/10/750,185 CURRENT FILING DATE: 2003-12-31 PRIOR PILING DATE: 2002-12-31 NUMBER OF SEQ ID NOS: 64922 SOFTWARE: Patentin Version 3.1 SEQ ID NO 35182 LENGTH: 1766
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US-10-750-185-35182
                      ROSENFELD, David
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89.50
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                                            HOLM, Tom
BATES, Stephen
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Query Match:
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                                            APPLICANT:
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Sequence 16, Application US/11038284

Publication No. US20050246793A1

GENERAL INFORMATION:

APPLICANT: COOKE, MICHAEL, JOHN

APPLICANT: GIDLEY, MICHAEL, JOHN

APPLICANT: SAFFORD, RICHARD

APPLICANT: SIDEBOTTOM, CHRISTOPHER, MICHAEL

APPLICANT: SIDEBOTTOM, CHRISTOPHER, MICHAEL

APPLICANT: WESTCOTT, ROGER, JOHN

TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION

FILE REPERENCE: 054163-5003-US.
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1198 GAGCTAGGAATIGTTGTTCTCATGGACATIGTTCACAGCCATGCATCAAATAATACTTTA 1257
                                                                                                                                                                                                                                                                                                  380 ProAlaCysPhelleThrGlnLeuLeuProValLysArgLysLeuGlyPheTyrGluTrp 399
                                                                                             ProLeu-----SerGlyLeuAlaTrpAlaValAla----MetIleAsnArgGlnGluIle 359
                                                                                                                                                                                                  360 GlyGlyProArgSerTyrThrIleAlaValAlaSerLeuGlyLysGlyValAlaCysAsn 379
ProLeuGlyLysGlnGlyTyrGlnLeuArgGlnGlyAspAsnPheGluValTrpGluArg 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 AlaAspProGlnArgPhe-----ProHisGlyIleArgGlnLeuAlaAsnTyrValHis 125
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Matches:
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CURRENT FILING DATE: 2005-01-21
PRIOR APPLICATION NUMBER: US/10/056,454
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: PCT/GB96/01075
PRIOR APPLICATION NUMBER: GB 9607409.1
PRIOR FILING DATE: 1996-05-03
PRIOR PILING DATE: 1996-04-10
PRIOR APPLICATION NUMBER: GB 9509229.2
PRIOR APPLICATION NUMBER: GB 9509229.2
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Query Match:
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|7222 CGCTGCCATGAAGCGGGACCGGCTGGCTTCCTGTCTCCTGGGTCGTCGCGACAGT 77281
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  ProLeu-----SerGlyLeuAlaTrpAlaValAla---MetIleAsnArgGlnGluIle 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 35, Application US/11112908
Publication No. US200502605591
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Beast Cancer Biomarkers
TITLE OF INVENTION: Breast Cancer Biomarkers
TITLE OF INVENTION: Breast Cancer Biomarkers
TITLE OF INVENTION: Breast Cancer Biomarkers
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT FILING DATE: 2004-04-23
PRIOR PILING DATE: 2004-04-3
PRIOR PILING DATE: 2004-06-10
PRIOR APPLICATION NUMBER: US 60/575,978
PRIOR FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR PILING DATE: 2004-11-30
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                                                                                                                        ---GlylleTyrAlaAspValGlyAsnLysThrCysAlaGlyPheProGlySerPheGly
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APPLICANT: Wang, Elizabeth
APPLICANT: Chen, C. M. Amy
APPLICANT: Shamah, Steven M.
TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
TITLE OF INVENTION: PROLIFERATION
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Mismatches:
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CURRENT APPLICATION NUMBER: US/11/108,528
CURRENT FILING DATE: 2005-04-18
FRIOR APPLICATION NUMBER: US 60/563,137
PRIOR FILING DATE: 2004-04-16
PRIOR PRIOR APPLICATION NUMBER: US 60/598,368
PRIOR FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 86
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 8501
                                                                                                                                                                                                              TyrTyrAspile --- AspAlaGlnThrPhe
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APPLICANT: SAFFORD, RICHARD
APPLICANT: SAFFORD, RICHARD
APPLICANT: SAFFORD, RICHARD
APPLICANT: SIDEBOTTON, CHRISTOPHER, MICHAEL
APPLICANT: WESTCOTT, ROGER, JOHN
TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
FILE REPERENCE: 044163-2603-012
CURRENT FILING DATE: 2002-01-24
FRIOR PAPLICATION NUMBER: US/10/056,454
FRIOR PAPLICATION NUMBER: PCT/GB96/01075
FRIOR APPLICATION NUMBER: GB 9607409.1
FRIOR APPLICATION NUMBER: GB 9607409.1
FRIOR APPLICATION NUMBER: GB 9509229.2
FRIOR PILING DATE: 1995-04-10
FRIOR FILING DATE: 1995-05-05
NUMBER OF SEQ ID NOS: 43
FRIOR FILING DATE: 1995-05-05
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| TATCATTGGATTCCCGCCTTTTTAACTATGGAAACTGGGAGGTACTTAGGTAT 1377
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      1258 GATGGACTGAACATGTTTGACGGCACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGT 1317
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                                             151 TyrTyrAspIle---AspAlaGlnThrPhe-----
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APPLICANT: DEBET, MARTINE
APPLICANT: GIDLEY, MICHAEL, JOHN
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; LOCATION: (24)..(2564)
US-11-038-284-19
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US-11-038-284-19
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LENGTH: 2578
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Best Local Similarity:
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                                                                                                                                                                            1034 CTACCAGGGAGCTGCTTTTTTTTTAGAAGGTTTTACCTTTAATGTTCTATTCATGGCCT 975
                                                                                                                                                                                                              128 ------GlyLeuLysLeuGlyIleTyr 134
                                                                                                                                                                                                                                               135 AlaAspyalGlyAsnLysThrCysAla---GlyPheProGlySerPheGlyTyrTyrAsp 153
                                                                                                                                                                                                                                                                                                                                                       154 IleAspAlaGlnThrPheAlaAspTrpGlyValAspLeuLeuLysPheAspGlyCysTyr 173
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                                                                    GlnArgPheProHisGlyIleArgGlnLeuAlaAsnTyrValHisSerLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GTCTGG 282
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US-1U-750-185-55673, Application US/10750185
; Sequence 55673, Application US/10750185
; Publication No. US20050603A1
; GENERAL INFORMATION:
; APPLICANT: WMI GENOMICS, INC.
; APPLICANT: WERR Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PATTIN Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; TULE REFERENCE: MMI1100-2
; CURRENT PAPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR PRILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SAFOND NOS 55673
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Conservative:
Mismatches:
Indels:
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; ORGANISM: Bovine 19866880894406
US-10-750-185-55673
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427 CGTGAACAAGTC------AAGGGGTGGAAAGGC------TTATTTTGCACT 465
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                                                                                                      RESULT 15
US-11-073-626-4

i Sequence 4, Application US/11073626

i Publication No. US20050244926A1

i GENERAL INFORMATION:
APPLICANT: KUROSMA, KEIKO
APPLICANT: KAIYAMA, KOZO
TITLE OF INVENTION: NOVEL FRUCTORY) peptide oxidase
FILE REPERENCE: 22759UNSO
CURRENT APPLICATION NUMBER: US/10/232,655
FRIOR APPLICATION NUMBER: US/10/232,655
PRIOR APPLICATION NUMBER: US/10/232,655
PRIOR APPLICATION NUMBER: US/10/232,655
PRIOR PILING DATE: 2001-09-04
PRIOR FILING DATE: 2001-09-04
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-12-12

RRIOR APPLICATION NUMBER: US 2002-228727

PRIOR FILING DATE: 2002-08-06

NUMBER: OF SEQ ID NOS: 24

SEQ ID NOS: 24

LENGTHER: PATCHTIN VEXBION 3.1

LENGTHER: DATE: 2002-08-06

LENGTHER: PATCHTIN VEXBION 3.1

LENGTHER: DATE: 2002-08-06

LENGTHER: PATCHTIN VEXBION 3.1
463 CCTCTCTTCTGCTCCAGCTCTGTGTTGGGACCTGGCT 501
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Matches:
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Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Eupenicillium terrenum
US-11-073-626-4
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Score:
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                                   703 GTTTCAAAGGCCTGGGTTTTCGCTCATATTCAACTCACACCCAAAGAAGCGGACGCGTAC
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Sequence 11, Application US/0993059;
Publication No. US20020088024A1
GENERAL INFORMATION:
APPLICANT: GRAGER, Stephen A.
APPLICANT: TUREEN, Thomas H.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
FILE REFERENCE: 008010087CPUS06;
CURRENT APPLICATION NUMBER: US/09/993,059;
CURRENT FILING DATE: 2001-11-13;
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
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US-10-103-327-7
US-10-602-219-7
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US-10-602-219-7
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US-10-984-389-7
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    TYPE: DNA ORGANISM: Homo sapiens
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      Command line parameters:
-MODEL=frame+_D2n.model -DBV=xlp
-Q=/Cogn2_1/USPTO epool_p/USPC062219/runat_23122005_151144_17253/app_query.fasta_1.583
-Q=/Cogn2_1/USPTO epool_p/USPC062219/runat_23122005_151144_17253/app_query.fasta_1.583
-DB=Published Applications NA Main -OFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1_-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 - TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN-0 -AALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAFSIZE=500 -MINILEN=0 -AALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAFSIZE=500 -MINILEN=0 -AALIGN=15 -MODE=LOCAL -OUTFMT=pto -LONGPG-6 -ICPU=3
-NO MAPP -LARGBGUERY -NEG-SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-NORMAP -LARGBGUERY -NEG-SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEC TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLOP=6 -DBLEXT=7
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Sequence 7, Appli
                                                                                                                                    December 26, 2005, 12:40:36; Search time 890 Seconds (without alignments) 3911.695 Million cell updates/sec
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1 MQLRNPELHLGCALALRFLA......RLRSHINPTGTVLLQLENTM 421
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2: /cgn2 6/ptodata1/pubpna/USOB-PUBCOMB.seq: *
3: /cgn2 6/ptodata1/pubpna/USOBA-PUBCOMB.seq: *
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                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-984-389-11
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1021 GAACGACCTCTCTCAGGCTTAGCCTGGGCTGTAGCTATGATAAACCGGCAGGAGATTGGT 1080
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                      GlyProArgSerTyrThrIleAlaValAlaSerLeuGlyLy8GlyValAlaCysAenPro
                                                                                 GCCTGCTTCATCATCACACACTCCTCCCTGTGAAAAGGAAGCTAGGGTTCTATGAATGGACT
                                                                                                                SerArgLeuArgSerHisIleAsnProThrGlyThrValLeuLeuGlnLeuGluAsnThr
                                                                     381 AlaCysPheIleThrGlnLeuLeuProValLysArgLysLeuGlyPheTyrGluTrpThr
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; Bedication No. US20030106095A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GARGER, Stephen A.
; APPLICANT: GARGER, Stephen A.
; TITLE OF INVENTION: PRODUCTION OF LXSOSOMAL ENZYMES IN
; TITLE OF INVENTION: PRODUCTION OF LXSOSOMAL ENZYMES IN
; TITLE OF INVENTION: PRODUCTION OF LXSOSOMAL ENZYMES IN
; TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
; FILE REFERENCE: 008010087CPUS06
; CURRENT APPLICATION NUMBER: US/10/103,327
; CURRENT APPLICATION NUMBER: US/09/993,059
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 37
; SOFIWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Homo sapiens
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Percent Similarity:
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NAME/KEY: CDS
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US-10-103-327-11
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Pred. No.:
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                                                                              AlaAsnTyzValHisSerLysGlyLeuLysLeuGlyIleTyzAlaAspValGlyAsnLys 140
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                                 MetGlnLeuArgAsnProGluLeuHisLeuGlyCysAlaLeuAlaLeuArgPheLeuAla
                                                                                                                              ThrMetGlyTrpLeuHisTrpGluArgPheMetCysAsnLeuAspCysGlnGluGluPro
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             US-10-602-219-12 (1-421) x US-09-993-059-11 (1-1266)
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US-10-602-219-11
; Sequence 11, Application US/10602219
; Publication No. US20040016021A1
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GENERAL INFORMATION:
APPLICANT: Large Scale Biology Corporation
APPLICANT: Turpen, Thomas H.
APPLICANT: Turpen, Thomas H.
APPLICANT: Erwin, Robert L.
APPLICANT: Gregory P.
APPLICANT: Grill, Laurence K.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZ
FILE REFERENCE: LSBC-0087-CP09B
CURRENT APPLICATION NUMBER: US/10/602,219
CURRENT PILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/930,059
PRIOR FILING DATE: 1090-05-26
PRIOR FILING DATE: 1994-10-14
PRIOR APPLICATION NUMBER: 08/314,003
PRIOR APPLICATION NUMBER: 08/314,003
PRIOR APPLICATION NUMBER: 08/314,003
PRIOR PILING DATE: 1994-10-14
PRIOR APPLICATION NUMBER: 07/997,733
PRIOR FILING DATE: 1992-12-29
PRIOR PILING DATE: 1992-12-29
PRIOR PILING DATE: 1992-07-31
PRIOR APPLICATION NUMBER: 07/60,244
PRIOR PILING DATE: 1990-10-22
PRIOR APPLICATION NUMBER: 07/601,244
PRIOR PILING DATE: 1991-01-16
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SEQ ID NO 11
LENGTH: 1266
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; ORGANISM: Homo sapiens
US-10-602-219-11
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APPLICANT: Erwin, Robert L.
APPLICANT: Grill, Laurence K.
ITILE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN PLANTS BY TRANIENT EXPRESSION
FILE REFERENCE: LSG-C0087-C0070
CURRENT APPLICATION NUMBER: US/410/602,220
CURRENT FILING DATE: 2011-11-13
PRIOR APPLICATION NUMBER: 09/93,059
PRIOR APPLICATION NUMBER: 09/93,059
PRIOR APPLICATION NUMBER: 09/16,127
PRIOR APPLICATION NUMBER: 09/16,72
PRIOR APPLICATION NUMBER: 09/16,72
PRIOR APPLICATION NUMBER: 09/16,144
PRIOR APPLICATION NUMBER: 08/176,414
PRIOR APPLICATION NUMBER: 08/176,414
PRIOR APPLICATION NUMBER: 08/176,414
PRIOR APPLICATION NUMBER: 08/176,414
PRIOR APPLICATION NUMBER: 07/99,733
PRIOR APPLICATION NUMBER: 07/93,733
PRIOR APPLICATION NUMBER: 07/93,692
PRIOR APPLICATION NUMBER: 07/600,244
PRIOR APPLICATION NUMBER: 07/600,244
PRIOR PLING DATE: 1992-01-13
PRIOR PLING DATE: 1992-01-14
PRIOR PLING DATE: 1991-01-16
PRIOR PRIOR PLING DATE: 1991-01-16
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                                            361 GCTAATTATGTTCACAGCAAAGGACTGAAGCTAGGGATTTATGCAGATGTTGGAAATAAA
                                                                                           421 ACCTGGGGGGTTCCCTGGGAGTTTTGGATACTACGACATTGATGCCCAGACCTTTGCT
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US-10-602-220-11
Sequence 11, Application US/10602220
Publication No. US20040023281A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Pred. No.:
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Percent Similarity: 1
Query Match:
BB:
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; LOCATION: (1)
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UG-10-851-388-11
; Sequence 11, Application US/10851388
; Publication No. US20040234516A1
; GENERAL INFORMATION:
; APPLICANT: GARGER, Stephen A.
; APPLICANT: TURPEN, Thomas H.
; APPLICANT: TURPEN, Monto H.
; TITLE OF INVENTION: PLANTE BY TRANSIENT EXPRESSION
; TITLE OF INVENTION: PLANTE BY TRANSIENT EXPRESSION
; FILE REFERENCE: 008010087CPUSO6
; CURRENT APPLICATION NUMBER: US/10/851,388
; CURRENT FILING DATE: 2004-05-21
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PRIOR APPLICATION NUMBER: US/09/993,059
PRIOR FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 11
LENGTH: 1266
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AGTATCTTGGACTGGACATCTTTTAACCAGGAGAAATTGTTGATGTTGCTGGACCAGGG
                       GlyTrpAsnAspProAspMetLeuValIleGlyAsnPheGlyLeuSerTrpAsnGlnGln
                                            781 GGTTGGAATGACCCAGATATGTTAGTGATTGGCAACTTTGGCCTCAGCTGGAATCAGCAA
                                                                       ValThrGlnMetAlaLeuTrpAlaIleMetAlaAlaProLeuPheMetSerAsnAspLeu
                                                                                     841 GTAACTCAGATGGCCCTCTGGGCTATCATGGCTGCTCCTTTATTCATGTCTAATGACCTC
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Publication No. US20050125859A1

GENERAL INPORMATION:

APPLICANT: GENERAL TRONE

APPLICANT: TURED: Stephen A.

APPLICANT: KUMAGAI, Monto H.

TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN

TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION

FILE REFERENCE: 008010087CPUS06

CURRENT APPLICATION NUMBER: US/10/984,389

CURRENT FILING DATE: 2004-11-08

PRIOR FILING DATE: 2001-11-13

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 1266
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; LOCATION: (1)
US-10-984-389-11
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US-10-984-389-11
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        201 SercysGluTrpProLeuTyrMetTrpProPheGlnLysProAsnTyrThrGluIleArg
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US-10-103-327-7
Sequence 7, Application US/10103327
Publication No. US20030106095A1
GENERAL INFORMATION:
APPLICANT: GARGER, Stephen A.
APPLICANT: TURPEN, Thomas H.
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US-09-93-059-7
is Sequence 7, Application US/09993059
is Publication No. US20020088024A1
is GENERAL INFORMATION:
APPLICANT: GARGER, Stephen A.
is APPLICANT: TURREN, Thomas H.
is APPLICANT: TURREN, THOMES H.
is TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION FILE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION CURRENT FILING DATE: 2001-11-13
is NUMBER OF SEQ ID NOS: 37
is SOFTWARE: PSELSEQ for Windows Version 4.0
is SEQ ID NO 7
is LENGTH: 1278
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Matches:
Conservative:
Mismatches:
Indels:
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1275)
US-09-993-059-7
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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DS-10-004-12-1

Sequence 7, Application US/10602219

Sequence 7, Application US/10602219

Fublication No. US20040016021A1

GENERAL INFORMATION

APPLICANT: Large Scale Biology Corporation

APPLICANT: Turpen, Thomas H.

APPLICANT: Pogue, Gregory P.

APPLICANT: Erwin, Robert L.

APPLICANT: Erwin, Robert L.

APPLICANT: Erwin, Robert L.

APPLICANT: Brain Robert L.

BRIOR APPLICANT: 1993-12-39

PRIOR APPLICANT: Brain Robert L.

BRIOR FILLING DATE: 1992-10-19

PRIOR FILLING DATE: 1992-10-19

PRIOR FILLING DATE: 1992-10-19

PRIOR FILLING DATE: 1992-10-19
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TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES ITILE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION FILE REFERENCE: 008010087CPUS06
CURRENT APPLICATION WUMBER: US/10/103,327
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: US/09/993,059
PRIOR APPLICATION NUMBER: US/09/993,059
RIOR FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches:
Conservative:
Mismatches:
Indels:
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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; LOCATION: (1)
US-10-103-327-7
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GENERALL INFORMATION:
APPLICANT: Large Scale Biology Corporation
APPLICANT: Large Scale Biology Corporation
APPLICANT: Large Scale Biology Corporation
APPLICANT: Turpen, Thomas H.
APPLICANT: Erwin, Robert L.
APPLICANT: BOOUCTION OF INSOME ENCYMES IN PLANTENT EXPRESSION
CURRENT FILIK DATE: 2003-6-23
CURRENT FILIK DATE: 2001-11-13
FRIOR APPLICATION NUMBER: 09/626,127
FRIOR APPLICATION NUMBER: 09/626,127
FRIOR APPLICATION NUMBER: 09/16,572
FRIOR APPLICATION NUMBER: 09/16,572
FRIOR APPLICATION NUMBER: 09/16,414
FRIOR FILING DATE: 1994-10-14
FRIOR FILING DATE: 1994-10-14
FRIOR FILING DATE: 1994-01-19
FRIOR FILING DATE: 1994-01-19
FRIOR FILING DATE: 1994-01-19
FRIOR FILING DATE: 1992-07-31
FRIOR FILING DATE: 1992-07-31
FRIOR APPLICATION NUMBER: 07/923,692
FRIOR FILING DATE: 1992-07-31
FRIOR FILING DATE: 1990-10-22
FRIOR FILING DATE: 1991-01-16
FRIOR FILING DATE: 1991-01-16
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                                        GlyProArgSerTyrThrIleAlaValAlaSerLeuGlyLyBGlyValAlaCysAsnPro
    721 AGTATCTTGGACTGGACATCTTTTAACCAGGAGAATTGTTGATGTTGCTGGACCAGGG
                                                                                                                    ValThrGlnMetAlaLeuTrpAlaIleMetAlaAlaProLeuPheMetSerAsnAspLeu
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PRIOR APPLICATION NUMBER: 07/600,244
PRIOR FILING DATE: 1990-10-22
PRIOR APPLICATION NUMBER: 07/641,617
PRIOR APPLICATION NUMBER: 07/641,617
PRIOR FILING DATE: 1991-01-16
PRIOR FILING DATE: 1991-01-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.2
SEQ ID NO 7
LENGTH: 1278
TYPE: DNA
CREANIESH: Homo sapiens
US-10-602-219-7
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                      GlnAspProLeuGlyLysGlnGlyTyrGlnLeuArgGlnGlyAspAsnPheGluValTrp
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US-10-851-388-7
; Sequence 7, Application US/10851388
; Publication No. US20040234516A1
; GENERAL INFORMATION:
; APPLICANT: GARGER, Stephen A.
; APPLICANT: TURPEN, Thomas H.
; APPLICANT: TURPEN, Thomas H.
; TITLE OF INVENTION: PRODUCTION OF LYSOSOWAL ENZYMES IN
; TITLE OF INVENTION: PRODUCTION OF LYSOSOWAL ENZYMES IN
; TITLE OF INVENTION: PLANTS CONTINUED OF TRANSIENT EXPRESSION
; FILE REPERENCE: 2004-00-21
; CURRENT APPLICATION NUMBER: US/10/851,388
; CURRENT APPLICATION NUMBER: US/09/993,059
; PRIOR PILING DATE: 2001-11-13
; NUMBER OF ERQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1278
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ORGANISM: Homo sapiens
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; Remaining Prior Application data rer; NUMBER OF SEQ ID NOS: 32; SOFTWARE: Patentin version 3.2; SEQ ID NO 7; LENGTH: 1278; TYPE: DNA ; ORGANISM: Homo sapiens
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                                                                                                                  Sequence 7, Application US/10984389;
Publication No. US20050128659A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GARGER, Stephen A.
APPLICANT: TURPEN, Thomas H.
TILLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN TITLE OF INVENTION: PRIANTS BY TRANSIENT EXPRESSION FILE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION FILE OF INVENTION NUMBER: US/10/984,389;
CURRENT APPLICATION NUMBER: US/09/993,059;
PRIOR FILING DATE: 2001-11-13;
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
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; LOCATION: (1)...(1275)
US-10-984-389-7
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Percent Similarity: 1
Best Local Similarity: 1
Query Match: 9
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FILE REFERENCE: 008010087CPUSO6
CURRENT APPLICATION NUMBER: US/09/993,059
CURRENT FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 1284
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Best Local Similarity:
Query Match:
DB:
                                                                  TYPE: DNA
ORGANISM: Homo
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NAME/KEY: CDS
LOCATION: (1).
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AlaAspGlyTyrLysHisMetSerLeuAlaLeuAsnArgThrGlyArgSerIleValTyr
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Publication No. US20020088024A1
GENERAL INFORMATION:
APPLICANT: GARGER, Stephen A.
APPLICANT: TUREEN, Thomas H.
APPLICANT: RUMAGAI. MONTO H.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES:
TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION
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                                                                  CAGTACTGCAATCACTGGCGAAATTTTGCTGACATTGATGATTCCTGGAAAAGTATAAAG 720
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                      MetGlnLeuArgAsnProGluLeuHisLeuGlyCysAlaLeuAlaLeuArgPheLeuAla
                                TrpLysAspAlaGlyTyrGluTyrLeuCysIleAspAspCysTrpMetAlaProGlnArg
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 (1-1284)
 US-10-602-219-12 (1-421) x US-10-103-327-13
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GlyTrpAsnAspProAspMetLeuValileGlyAsnPheGlyLeuSerTrpAsnGlnGln
                                                                                             GTAACTCAGATGGCCCTCTGGGCTATCATGGCTGCTCTTTATTCATGTCTAATGACCTC
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                                               GGTTGGAATGACCCAGATATGTTAGTGATTGGCAACTTTGGCCTCAGCTGGAATCAGCAAA
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; Sequence 13, Application US/10103327
; Publication No. US20030106095A1
; Publication No. US20030106095A1
; GENERAL INVEMATION:
; APPLICANT: GARGER, Stephen A.
; APPLICANT: TURREN, THOMASH H.
; TITLE OF INVENTION: PRODUCTION OF LYSOSOWAL ENZYMES IN
; TITLE OF INVENTION: PRANTE BY TRANSIENT EXPRESSION
; FILE REFERENCE: 008010087CFUSOG
; CURRENT APPLICATION NUMBER: US/10/103,327
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US/09/993,059
; PRIOR RELIGN DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PSESSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1284
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Best Local Similarity:
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NAME/KEY: CDS
LOCATION: (1).
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21 LeuValSerTrpAspIleProGlyAlaArgAlaLeuAspAsnGlyLeuAlaArgThrPro 4 61 CTGGTTCCTGGGACATCCCTGGGCTAGAGCACTGGACAATGGATTGGCAAGGACGCCT 1 61 ThrMetGlyTrpLeuHisTrpGluArgPheMetCysAsnLeuAspCysGlnGluGluBro 6 61 AspSerCysIleStGluLySLeuPheMetGluMetAlaGluLeuMetValSerGluGly 8 61 AspSerCysIleStGluLySLeuPheMetGluMetAlaGluLeuMetValSerGluGly 8 61 AspSerCysIleStGluLySLeuPheMetGluMetAlaGluLeuMetValSerGluGly 8 62 AspSerCysIleStGluLySLeuPheMetGluMetAlaGluLeuMetValSerGluGly 8 63 ATTCCTGCATCAGTGAGAAGCTCTTCATGGAGATGGCAGGAGCTCCATGGTCCAGAAGGC 2 64 AspSerCysIleAspAspCysTrpMetAlaProGlnArg 1 65 AspSerCysIleAspAspCysTrpMetAlaProGlnArg 1 66 AspSerCysIleAspAspCysTrpMetAlaProGlnArg 1	Db 241 TGGAAGGATGCAGGTTATGAGTACTCTGCATTGATGACTGATGATGATGATGATGATGATGATGATGATGATGATGAT	1081 GGACCTCGCTCTTATACCATCGCAGTTGCTTCCCTGGGTAAAGGAGTGGCCTGTAATCCT 1
361 GlyE 1081 GGAC 381 Alac 1141 GCCI 401 Seri 1201 TCAE 421 Met	1261 ATG 1263 110-602-139-13	Qy 1 MetGlnLeuArgAsnProGluLeuHisLeuGlyCysAlaLeuArgPheLeuAla 20

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- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                      AY408542 I
CO645672 II
CT005156 C
CT005156 C
CO646251 II
CO646251 II
CO646251 II
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CO64623 A
BU596617 A
BUS96617 A
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CD385342 I
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full-length cDNA clone CS0DB008YB11 of Neuroblastoma Cot
10-normalized of Homo sapiens (human).
                   ALS52630 BMS64282 BQ062192 CO645623 ALS77581
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1 (bases 1 to 1277)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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            GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                    nucleic search, using frame plus p2n model
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Database :

Score

Result Š. 2314 2309 2289 2104 2055 1811

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Submitted (20-JUL 2004) Genoscope - Centre National de Sequencage: Submitted (20-JUL 2004) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr) and ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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1 (bases 1 to 1266)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
GETTGGAATGACCCAGATATGTTAGTGATTGGCAACTTTGGCCTCAGCTGGAATCAGCAA
                                           ArgHislleSerProGlnAlaLysAlaLeuLeuGlnAspLysAspVallleAlaIleAsn
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue
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/mol_type="mRNA"
/mol_type="taxon:9606"
/clone="CSODI067Y001"
/tissue_type="Placenta Cot 25-normalized"
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Matches:
Conservative:
Mismatches:
Indels:
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/db_xxef="taxon:9606"
/clone="CSODBO08YB11"
/tissue_type="Neuroblastoma_CC/plasmid="pcMVSPORT_6"
                                                                                                                                                                                                                                       Gaps:
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   Location/Qualifiers
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Direct Submission
Submitted (20-JUJ-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invirogen.
                                                                                                       1146
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1 (bases 1 to 1253)

1 ii, W B., Gruber, C., Jessee, J. and Polayes, D. Pull-length cDNA libraries and normalization
Unpublished
Contact: Feng Liang Email: fliangalifetech.com URL: thtp://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue.

2 (bases 1 to 1253)
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/tissue type="Heia cells Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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Matches:
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CR617861.1 GI:50498668
HTC; CNSLT_CDNA.
HOMO SAPIENB (human)
HOMO SAPIENB
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                             Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                           2.27e-242
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Homo sapiens GLA gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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1 (Dases 1 to 1290)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Ferritera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
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(Dases 1 to 1290)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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               GlyProArgSerTyrThrIleAlaValAlaSerLeuGlyLysGlyValAlaCysAsnPro
                               1086 GGACCTCGCTCTTATACCATCGCAGTTGCTTCCCTGGGTAAAGGAGTGGCCTGTAAATCCT
                                                                                        MetGlnLeuArgAsnProGluLeuHisLeuGlyCysAlaLeuAlaLeuArgPheLeuAla
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                                                                          AlaCysPhelleThrGlnLeuLeuProValLysArgLysLeuGlyPheTyrGluTrpThr
                                                                                                                                   401 SerArgLeuArgSerHisIleAsnProThrGlyThrValLeuLeuGln 416
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Matches:
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/db_xref="taxon:9606"
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                            MetGlnLeuArgAsnProGluLeuHisLeuGlyCysAlaLeuAlaLeuArgPheLeuAla
                                                       ATGCAGCTGAGGAACCCAGAACTACATCTGGGCTGCGCGCTTGCGCTTCGCTTCCTGGCC
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1290 bp DNA linear GSS 15-DEC-2003
Pan troglodytes GLA gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
1201 TCAAGGTTAAGAAGTCACATAAATCCCACAGGCACTGTTTTGCTTCAGCTAGAAAATACA 1260
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I (bases 1 to 1290)
Clark, A.G. Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Territara, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, White, T.J., Sninsky, J.J.,
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submitsation
Direct Submitsation
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
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/locus_tag="HCM3258"
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AKO54547 AKO54547 Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN Full-length enriched library, clone:E330039008 product:galactosidase, alpha, full insert sequence. AKO54547 AKO54547 Mus musculus (house mouse) Mus musculus (house mouse) Mus musculus (house mouse) Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning		Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi Yujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watshikaya, Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawa Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. FUNCTIONAL annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001) The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)		Muramatsu, M. and Hayashizaki,Y. Direct Submission Submitted (16-UTU-2011) Yoshihi Physical and Chemical Research Exploration Research Group, RIKEN Yokohama Institute, 1-7-2; Kanagawa 230-0045, Japan (E-mai: URL:http://genome.gsc.riken.jp/	raxial-45-500-7410) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
RESULT 6 AK054547 LOCUS DEFINITION ACCESSION VERSTON KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE	PUBNED PUBNED AUTHORS TITLE JOURNAL PUBNED REFERENCE AUTHORS	TITLE JOURNAL PUBMED REFERENCE	AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOIRNAL	REFERENCE AUTHORS	TITLE JOURNAL	COMMENT
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Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed typepare mouse tissues.
Please visit our web gite for further details.
URL:http://genome.gsc.riken.jp/.
URL:http://fantom.gsc.riken.jp/.
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AND MUS MUSCULUS 0 day neonate thymus CDNA, RIKEN full-length enriched library, clone:A430057F16 product:galactosidase, alpha, full insert sequence.
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                                                                                                             AspIrpGlyValAspLeuLeuLysPheAspGlyCysTyrCysAspSerLeuGluAsnLeu 180
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HTC; CAP trapper.
HTC and susculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                               627 TCCTGTGAGTGGCCACTTTATTTGAGACCCTTTCATAAGCCCAATTATACAGATATCCAA
                                                                                                                                                                                                                                                                                                                                         GlyTrpAsnAspProAspMetLeuVallleGlyAsnPheGlyLeuSerTrpAsnGlnGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               867 GIGACACAGAIGGCCCTCTGGGCTAICAIGGCCGCTCCCTACTCAIGICCAACGAICTG
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                                                                                                                                                                                                                                                                                                                    221 GlnTyrCysAsnHisTrpArgAsnPheAlaAspIleAspAspSerTrpLysSerIleLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ValThrGlnMetAlaLeuTrpAlaIleMetAlaAlaProLeuPheMetSerAsnAspLeu
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                                                                                                               galactosidase, alpha
evidence: BLASTN, 99%,
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41
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Conservative:
Mismatches:
Indels:
                                                                                                                  protein product;
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1811.00
88.04%
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length, cDNAs

Nature 420, 563-573 (2002)

E (bases 1 to 2962)

Adachi, J., Aizawa, K., Akimura, T., Hara, A., Hashizume, W.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramco, K., Hirackar, T., Hirozane, T.,
Hori, F., Imotani, K., Ishi, Y., Itoh, M., Kagawa, T., Kasukawa, T.,
Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
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Nakamura, M., Nishi, K., Saitoh, H., Sakai, K., Ohno, M., Ohaeto, N.,
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Sogabe, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramateuu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Exploration Research Group, RIKEN Genome Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-resegec:riken:Jp,
URL:http://genome-gsc.riken:Jp/, Tel:81-45-503-9216)
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN
Division of Experimental Animal Research in Riken
                                                                                                                                                                                  Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                          Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Sumamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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/db_xref="taxon:10090"
                                                                Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr. Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMYSORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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AL554978 GI:45859723 GI:45859723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODK009BC06QP1&c=10506.r.
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1 (bases 1 to 1086)

Lii.W.B., Gruber,C., Jessee,J. and Polayes,D.

Lull.length cDNA libraries and normalization
Unpublished (2001)
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Homo sapiens
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241 SerileteukepTrpThrSerPheAsnGinGluArgileValApValAlaGlyProGly 260 Db 725 AGTATCTTGGACGACATTTTACCAGGAGAATTTTTGATGGTGGACGGGG 784 CV 261 GlyTrpAsnAspProAspWetLeuVallaGlyAndrpTGATTGGTGGACGGGG 784 CM 281 ValThrGlaWetAlaLeuTrpAlalie-WetAlaAlaProLeupheWeiSerTrpAsnGinGin 280 Db 845 GTACTCAGATGCCCCTGGGGATATTCATGGCTCTCACTGGTGAATGCCAGGGAATTGCCAGTGGAATGCCAGGGAATTGCCAGTGGAATGCCAGGGAATGCCAGGTGGAATGCCAGGTGAATGCCAGTGGAATGCCAGTGGAATGCCAGTGGAATGCCAGTGGAATGCCAGTGGAATGCCAGTGGAATGCCAGTGGAATGCCAGTGGAATGCCAGTGGAATGCCAGTGGAATGCAGGGAATGCAGGCTCTCATTGATCAGGTGAATGCCAGGGAATGCAGGCTCTCATTGATCAGGTGAATGCCAGTGGAATGCAGGGTGAATGCAGGTGGAATGCAGGGAATGCAGGCTCTCATTGATCAGGTGAATGCCAGGGAATGCAGGCTCTCAGGATGCAGGTGAATGCAGGTGAATGCAGGAATGCAGGATGCAGGGTGAGTGA	FEATURES Location/Qualifiers Location/Qualifiers Source http://www.genoscope.cns.fr/cdna?s=CSODCO14DD02QP1&c=10506.r. Location/Qualifiers 11014 /organism="Homo sapiens" /mol_type="mxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

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BMS64282
AGENCOURT_6560104 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742198
5', mRNA sequence.
BMS64282
BMS64282. GI:18811955
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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I (bases 1 to 1067)

II (bases 1 to 1067)

INH-WGC http://mgc.nci.nih.gov/.

NALional Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Contact: Robert Strausberg, Ph.D.

Email: clapsb-remail.nih.gov

Contact: Natayed by: The I.M.A.G.E. Consortium (LINL)

DNA bequencing by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
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                                                                         AlaAsnTyrValHisSerLysGlyLeuLysLeuGlyIleTyrAlaAspValGlyAsnLys
                                                                                                                                                             ThrCysAlaGlyPheProGlySerPheGlyTyrTyrAspIleAspAlaGlnThrPheAla
                                                                                                                                                                                  AspTrpGlyValAspLeuLeuLysPheAspGlyCysTyrCysAspSerLeuGluAsnLeu
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                                       garrcagaaggcagacrrcaggcagccrcagggcrrrrccrcarggarrcgccagcra
                                                                                                                     366 GCTAATTATGTTCACAGCAAAGGACTGAAGCTAGGGATTTATGCAGATGTTGGAAATAAA
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15. 1 (Dases 1 to 999)

16. Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

17. Li, Gruber, C., Jessee, J. and Polayes, D.

18. Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

19. Full-length cDNA libraries and normalization

19. To provide the sequence version replaced gi:31274445.

19. Contact: Genoscope

2 rue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE

2 rue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE

Email: seqref@genoscope.cns.fr. Web: www.genoscope.cns.fr

18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCWVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster
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                    ALS52630
ALS52630 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI067XJ01 5-PRIME, mRNA sequence.
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sites of the pCMVSPORT 6 vector. Library was normalized."
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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http://www.genoscope.cns.fr/cdna?s=CSODI067CE01QP1&c=10506.r.
Location/Qualifiers
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/db_xref="taxon:9606"
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Homo sapiens
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Best Local Similarity:
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ACTIVITY 6829871 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5923640
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E 1 (bases 1 to 1005)
S NIH-Mac http://mac.nci.nih.gov/.
S NIH-Mac http://mac.nci.nih.gov/.
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabbe-remail.nih.gov
Tissue Procurement: Low Standt
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCNZ092 row: h column: 09
High quality sequence stop: 676.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                  616 GAGTGGCCTCTTTATATGTGGCCCTTTCAAAAGCCCAATTATACAGAAATCCGACAGTAC
                         GluTrpProLeuTyrMetTrpProPheGlnLysProAsnTyrThrGluIleArgGlnTyr
                                                                                                            CysAsnHisTrpArgAsnPheAlaAspIleAspAspSerTrpLysSerIleLysSerIle
                                                                                                                                     rGlnMetalaLeuTrpalaIleMetalaala-ProLeuPheMetSerAsnAspLeuArgH
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Homo sapiens
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// not2="Organ: brain; Vector: pCMV-SPORT6; Site 1: Not1;
// not2="Organ: bcm, vector: pCMV-SPORT6; Site 1: Not2: pCMMC, pCMMC, vector: p
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found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM12759 row: p column: 07
High quality sequence stop: 761.
Location/Qualifiers
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GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) sing ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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Matches:
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Email: cmagness@illumigen.com
Email: cmagness@illumigen.com
Sequenced on 2004.03.02. 796 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.

[ (Dases I to 92.)

Magness, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B., Proll, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. ar Iadonato, S.P.
                                                                                                                                                                                                                                                                                      CO645623 922 bp mRNA linear EST 23-JUL-2(
LLUMYGEN MCQ 24642 Katze MMLV Macaca mulatta cDNA clone
IBIUW:23923 5' similar to Bases 5 to 920 highly similar to human
GLA (Hs.69089), mRNA sequence.
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/lab_host="Electromax DH10B"
/clone lib="Katze=mMLV"
/note="Organ: liver; Vector: pDONR 222; Site_1: BsrG I;
Site_2: BsrG I; Created from CloneMiner cDNA_Library
Construction kit (catalog #18249-029)"
Analysis of the Macaca mulatta transcriptome and the sequence divergence between Macaca and human Genome Biol. 6 (7), R60 (2005)
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Conservative:
Mismatches:
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Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle,
Tel: 2063780400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.macaque.org
PCR PRimers
FORWARD: CCCTCACTAAAGGGAACAAAA
BACKWARD: CACTATAGGGCGAATTGGGTA
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/mol_type="mRNA"
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/clone="IBIUW:23923"
/sex="female"
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Macaca mulatta
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ACCESSION AL577581.3 GI:46256603 KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM Homo sapiens Hominidae; Homo. Hominidae; Homo. Hominidae; Homo. Ii,W.B., Gruber,C., Jessee,J. and Polayes,D. ATTHLE TITLE FUll-length cDNA libraries and normalization JOURNAL COMMENT CONTEACT: Genoscope Genoscope - Centre National de Sequencage Genoscope - Centre	FRATURES http://www.genoscope.cna.fr/cdnafs=CSODKOO9BCO6NP1&c=10506.r. Location/Qualifiers 1. 1026 /organism="Homo sapiens" /mol_type="mRNA" /do xref="taxon:9606" /clone="CSODKOO9YE12" /cell_type="HELA CELLS COT 25-NORMALIZED" /cell_type="HELA" /clone="HELA" /clone="Lib="HELA" /clone="Lib="HELA" /clone="Lib="HELA" /clone="Lib="HELA" /clone="lib" /cl	Alignment Scores: 6.5e-170 Length: 1026 Pred. No.: 1648.50 Matches: 308 Score: 1648.50 Matches: 1 Best Local Similarity: 98.09\$ Mismatches: 5 Query Match: 1.24\$ Indels: 2 DB: 1		Db 897 ATTGGCAGCTAGTTATGTTCACAGCAAAGGACTGAAGGATTTATGCAGAT 838 Qy 137 ValGlyAbnLy8ThcCysalaGlyPheProGlyCsrPheGlyTyTTyTASpIleAspAla 156 Db 837 GTTGGAAATAAAACCTGCGCAGGCTTCCCTGGAGTTTTGGATACTACGACATTGATGC 778 Qy 157 GINThrPheAlaAspTrpGlyValAspLeuLeuLy8PheAspGlyCy8TyTCy8AspSer 176 Db 777 CAGACCTTTGCTGACTAGATACATCGCTAAAATTTGATGGTTGTTACTGTGACAGT 718	Qy 177 LeuGludsnLeualadspGlyTyrLysHisMetSerLeualaLeuasndrgThrGlydrg 196
Query Match: 71.26* Indels: 0 DB: 7 Gaps: 0 US-10-602-219-12 (1-421) x CO645623 (1-922) 0 1 MetGlnLeuargAsnProGluLeuHisLeuGlyCysAlaLeuAlaLeuArgPheLeuAla 20 11 ATGCAGCTGAGGAACCCAGAAATGCATCTGGGCTGCGCGTTCTCTTCTTCTGGCC 70 Qy 21 LeuValSeTTpAspIleProGlyAlaArgAlaLeuAspAsnGlyLeuAlaArgThrPro 40 Phill	Qy 101 AspSerGluGlyArgLeuGlnAlaAspProGlnArgPheProHisGlyIleArgGlnLeu 120 Db 311 GATTTAGAAGGCAGACCTCAGCGCTTTCCTCATGGGATTCGCCAGCTA 370 Qy 121 AlaAsnTyrValHisSerLyGGlyLeuLysLeuGlyIleTyrAlaAspValGlyAsnLys 140 Db 371 GCTAATTATGTTCACAGGATGAGGTTAGGGATTATGCGATGTTGGAAATAAA 430 Qy 141 ThrCysAlaGlyPheProGlySerPheGlyYyrTyrAspIleAspIlaGlnThrPheAla 160 Db 431 ACCTGCGCAGGCTTCCTGGGAGTTTTGGATACTTAGCCCAGACCTTTGT 490 Qy 161 AspTrpGlyValAspLeuLeuLeuLySPHeAspGlyCysTyrCysAspSerLeuGluAsnLeu 490 Qy 161 AspTrpGlyValAspLeuLeuLeuLySPHeAspGlyCysTyrCysAspSerLeuGluAsnLeu 180 Qy 161 AspTrpGlyValAspLeuLeuLeuLySPHeAspGlyCysTyrCysAspSerLeuGluAsnLeu 180 Qy 161 AspTrpGlyValAspLeuLeuLeuLySPHeAspGlyCysTyrCysAspSerLeuGluAsnLeu 180 A91 GACTGGGGGGTAGATCTGAAATTTGAAGGTTGTGACAGTTTGGAAAAATTGGAAAAATTGGAAAAATTGGAAAAATTTGAAAAATTTGAAAAATTTGAAAAAA	Qy 181 AlaAspGlyTyrLysHisNetSerLeuAlaLeuAsnargThrGlyArgSerIleValTyr 200 Db 551 GCAGATGGTTATAAGCACTGTCCTTGGCCCTGAATAGGACTGGCAGAAGCATTGTGTAC 610 Qy 201 SerCysGluTrpProLeuTyrMetTrpProPheGlnLysProAsnTyrThrGluIleArg 220 Db 611 TCCTGTGAGTGGCCTCTTTATATGTGGCCATTTCAAAAGCCCAATTACACAGAAATCCGA 670	Qy 221 GlnTyrCysAsnHisTrpArgAsnPheAlaAspIleAspAspSerTrpLysSerIleLys 240 Db 671 CAGTACTGCAATCACTGGCGAAATTTTGCTGACATTGATGATTCCTGGAAAAGTATAAAG 730 Qy 241 SerIleLeuAspTrpThrSerPheAsnGlnGluArg1leValAspValAlaGlyProGly 260 Db 731 AGTATCTTGGACTGGACATCTTTTAACCAGGAGAAATTGTTGATGTTGCTGGACCAGGG 790	Cy 261 GlyTrpAsnAspProAspMetLeuValIleGlyAsnPheGlyLeuSerTrpAsnGlnGln 280	Db 911 CGACACATCACC 922 RESULT 14 AL577581/c LOCUS AL577581 Homo sapiens HELA CELLS COT 25-NORWALIZED Homo sapiens

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1 (bases 1 to 1296)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Ferriera, S., Wanphy, B., Ferriera, S., Wanp, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
Fockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
                        PheGluValTrpGluArgProLeuSerGlyLeuAlaTrpAlaValAlaMetlleAsnArg
                                                                                                                                                                                                                                  SerAsnAspLeuArgHisIleSerProGlnAlaLysAlaLeuLeuGlnAspLysAspVal
                                                                                                                                                                                                                                                357 TCTAATGACCTCCGACACATCAGCCCTCAAGCCAAAGCTCTCCTTCAGGATAAGGACGTA
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Conservative:
Mismatches:
Indels:
Gaps:
them based on alignment.

Location/Qualifiers

1.1296

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                                                                    341 GluargProLeuSerGlyLeualaTrpalaValalaMetIleAsnargGlnGluIleGly 360
261 GlyTrpAsnAspProAspMetLeuVallleGlyAsnPheGlyLeuSerTrpAsnGlnGln 280
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AD084746
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-MODEL=frame+ p2n.model -DEV=xlp
-Q=/Cogn_2 1/05PTO spool p/USIO1602219/runat 23122005 151141 17129/app_query.fasta_1.583
-Q=/Cogn_2 1/05PTO spool p/USIO1602219/runat 23122005 151141 17129/app_query.fasta_1.583
-DB=N Geneseq -OFMT=fastap -SUFFTX=p2n.rng -MINNATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS_Ebits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=ptco -NORM=ext -HEAPSIZE=50 -MINLEN=0 -MAXLEN=20000000000
-USER=USIO602219 @CGN 1 1 1096 @runat 2312005 151141 17129 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV TINROUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7
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Add84750 Human alp
Adj88276 Human WT
Adm48680 Human wil
                                                                                                                                                            December 26, 2005, 08:34:41 ; Search time 666 Seconds (without alignments) 4212.966 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                 1 MQLRNPELHLGCALALRFLA......RLRSHINPTGTVLLQLENTM 421
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                         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
                                                                                                                    nucleic search, using frame_plus_p2n model
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Listing first 45 summaries
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ADM48680
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                        GCAGATGGTTATAAGCACATGTCCTTGGCCCTGAATAGGACTGGCAGAAGCATTGTGTGTAC
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                                                                                                       GlnTyrCysAsnHisTrpArgAsnPheAlaAspIleAspAspSerTrpLysSerIleLys
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                                                                    SerileLeuAspTrpThrSerPheAsnGlnGluArg1leValAspValAlaGlyProGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; alpha-galactosidase; rGAL-4; gene; ds; lysosomal enzyme; enzyme replacement therapy; lysosomal disease.
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/product= "Human rGAL-8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human alpha-galactosidase rGAL-8 DNA.
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                                                                                                                                                             The invention relates to human alpha-galactosidase truncated at the carboxy terminus and the production of enzymatically active recombinant human and animal lysosomal enzymes. The invention is useful for producing lysosomal enzymes for treating lysosomal storage diseases, producing altered or mutated proteins, enzymatically active or otherwise, to serve as precursors or substrates for further in vivo or in vitro processing to a specialised industrial form for research or therapeutic uses, to produce more effective therapeutic enzyme, for producing antibodies against lysosomal enzymes for medical diagnostic use, and in any sequence is human rGAL-8 DNA
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GARGER S J.
TURPEN T H.
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P-PSDB; AAE28210.
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Fabry's disease; Gaucher's disease; human; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to human alpha-galactosidase derivatives and the nucleic acids encoding them. The polypeptides are used in a method for producing active recombinant human and animal lysosomal enzymes in a plant expression system. The enzymes can be used in enzyme replacement therapy for the therapeutic treatment of human and animal lysosomal diseases. This sequence represents DNA encoding a human alphagalactosidase derivative polypeptide of the invention.
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                                                                                                                                         (GARG/) GARGER S J.
(TURP/) TURPEN T H.
(KUMA/) KUMAGAI M H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to nucleotide encoding galactosidase (GAL). The hivention is useful in gene therapy. The polymucleotides and polypeptides are useful in treating human and animal lysosomal storage diseases, e.g. Fabry's disease and Gaucher's diseases. The present sequence is human GAL
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                                         /product= "Human WT
          Location/Qualifiers
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91US-00739143.

92US-0093733.

92US-0019414.

91US-00131637.

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P-PSDB; ADJ88277.
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ERWIN R L.
GRILL L K.
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Best Local Similarity:
                                                             US2004016021-A1
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08-JUN-1989;
22-OCT-1990;
16-JAN-1991;
26-JUL-1991;
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31-JUL-1992;
30-DEC-1992;
29-DEC-1993;
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to novel galactosidase (Gal) proteins such as rGAL-12, rGAL-12R, r-GAL-25 or rGAL-25R. The methods and compositions of the present invention are useful for producing recombinant lysosomal enzymes for enzyme replacement therapy for treating human and animal lysosomal storage diseases as as Gauchas, si disease, Niemann-Pick disease, Rabry disease and Tay-Sachs disease. The present sequence is human wild type rGAL-8 DNA used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New alpha-galactosidase polypeptides, useful in producing recombinant lysosomal enzymes for the treatment of lysosomal storage diseases, such as Gaucher's disease, Niemann-Pick disease, Fabry disease and Tay-Sachs
                                                                                                                                                                                                                                                                       Galactosidase; Gal; lysosomal enzyme; enzyme replacement therapy;
lysosomal storage disease; Gaucher's disease; Niemann-Pick disease;
Fabry disease; Tay-Sachs disease; cardiovascular; nephrotrophic; human;
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/product= "GAL-8
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17-FEB-1999; 89US-0016071.
22-OCT-1992; 90US-00500244.
31-UIL-1992; 92US-00997733.
29-DEC-1992; 93US-00176414.
19-JAN-1994; 94US-00176414.
14-OCT-1994; 94US-00134003.
21-MAY-1994; 94US-00316572.
26-UIL-2000; 2000US-00626127.
13-NOV-2001; 2001US-00993059.
                                                                                                                                     ADM48680 standard; DNA; 1266
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KUMAGAI M H.
POGUE G P.
ERWIN R L.
GRILL L K.
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17-FEB-1989;
22-OCT-1990;
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lysosomal enzymes in plants by a transient plant expression system. The invention relates to glucocerebrosidase (GCB, GCR) and alphagalactosidase enzymes having a post-translational modification provided by the plant expression system. The invention is useful in enzyme replacement therapy for treating lysosomal storage diseases such as Gaucher's disease, Niemann-Pick disease, Pabry's disease and Tay-Sachs disease, Hurler's syndrome and Hurler-Scheie syndrome. The invention is also useful in researches for developing new approaches to medical treatment of lysosomal storage diseases and in industrial processes involving enzymatic substrate hydrolysis. The present sequence is the human alpha-galactosidase protein encoding DNA.
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  961 CAGGACCCCTTGGGCAAGCAAGGGTACCAGCTTAGACAGGGAGACAACTTTGAAGTGTGG
                                                                                                                                                    GluArgProLeuSerGlyLeuAlaTrpAlaValAlaMetIleAsnArgGlnGluIleGly
                                                                                                                                                                               GlyProArgSerTyrThr1leAlaValAlaSerLeuGlyLysGlyValAlaCysAsnPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A pharmaceutical composition comprising a lysosomal enzyme, useful enzyme replacement therapy for the treatment of lysosomal storage diseases, such as Fabry's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to the production of human and animal
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1. .1266
/*tag= a
/product= "Human alpha-galactosidase protein"
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13-NOV-2001; 2001US-00993059.
20-MAR-2002; 2002US-00103327.
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P-PSDB; ADU66916.
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                                                                                                                                                                                                                                                                                                                                                                                                  ArgHis1leSerProGlnAlaLysAlaLeuLeuGlnAspLysAspVal1leAlaIleAsn
                                                                                                                                                                                                                                                             GlnAspProLeuGlyLysGlnGlyTyrGlnLeuArgGlnGlyAspAsnPheGluValTrp
GlyTrpAsnAspProAspMetLeuValIleGlyAsnPheGlyLeuSerTrpAsnGlnGln
                                                                         GGTTGGAATGACCCCAGATATGTTAGTGATTGGCAACTTTGGCCTCAGCTGGAATCAGCAA
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13-NOV-2001; 2001US-00993059.
20-MAR-2002; 2002US-00103327.
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TrpLysAspAlaGlyTyrGluTyrLeuCysIleAspAspCysTrpMetAlaProGlnArg 100
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                                                                                                                                                                                                         e.9
                                                                                                                                                                                                                                                                                                                                            The present invention relates to the production of human and animal lysosomal enzymes in plants by a transient plant expression system. The invention relates to glucocerebrosidase (GGB, GCR) and alpha-tinvention relates to glucocerebrosidase (GGB, GCR) and alpha-tinvention relates to glucocerebrosidase (GGB, GCR) and alpha-tinvention and invention and in the provided by the plant expression system. The invention is useful in anymer replacement therapy for treating lysosomal storage diseases such as Gaucher's disease, Niemann-Pick disease, Fabry's disease, Tay-Sachs disease, Hurler's syndrome and Hurler-Scheie syndrome. The invention is also useful in researches for developing new approaches to medical treatment of lysosomal storage diseases and in industrial processes involving enzymatic substrate hydrolysis. The present sequence is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MetGlnLeuArgAsnProGluLeuHisLeuGlyCysAlaLeuAlaLeuArgPheLeuAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AspSerCysIleSerGluLysLeuPheMetGluMetAlaGluLeuMetValSerGluGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCTGCGCAGGCTTCCCTGGGAGTTTTGGATACTACGACATTGATGCCCAGACCTTTGCT
                                                                                                                                      New isolated polypeptides useful for producing lysosomal enzymes in plants to be utilized in enzyme replacement therapy or for the therapeutic treatment of human or animal lysosomal storage diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T; 0 U; 0 Other;
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Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 11; 88pp; English.
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   Kumagai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human alpha-galactosidase DNA
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2314.00
100.00%
100.00%
Turpen TH,
                                                      WPI; 2005-404004/41.
P-PSDB; AEA27445.
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                    Gaucher's disease
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The invention relates to human alpha-galactosidase truncated at the carboxy terminus and the production of enzymatically active recombinant human and animal lysosomal enzymes. The invention is useful for producing lysosomal enzymes for treating lysosomal storage diseases, producing altered or mutated proteins, enzymatically active or otherwise, to serve as precursors or substrates for further in vivo or in vitro processing to produce more effective therapeutic ensempth or therapeutic uses, to produce more effective therapeutic enzyme, for producing antibodies against lysosomal enzymes for medical diagnostic use, and in any commercial process that involves substrate hydrolysis. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AlaAsnTyrValHisSerLysGlyLeuLysLeuGlyIleTyrAlaAspValGlyAsnLys 140
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                                                                                                                                                                                                                                                                                  Novel human alpha-galactosidase polypeptide useful for treating lysosomal
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                                                                                                                                                                                              Kumagai MH
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                                                  13-NOV-2001; 2001US-00993059
                                                                                     26-JUL-2000; 2000US-00626127
                                                                                                                                                                                              Garger SJ, Turpen TH,
                                                                                                                      (GARG/) GARGER S J.
(TURP/) TURPEN T H.
(KUMA/) KUMAGAI M H.
                                                                                                                                                                                                                                WPI; 2002-681656/73
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Best Local Similarity:
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                                                                  SerCysGluTrpProLeuTyrMetTrpProPheGlnLysProAsnTyrThrGluIleArg
                                                                                                                                                                                                                                       721 AGTATCTTGGACTGGACATCTTTTAACCAGGAGAGAATTGTTGATGTTGCTGGACCAGGG
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                  GCAGATGGTTATAAGCACATGTCCTTGGCCCTGAATAGGACTGGCAGAAGCATTGTGTAC
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                                                                                                                                                                                                                                                                                    GlyTrpAsnAspProAspMetLeuValIleGlyAsnPheGlyLeuSerTrpAsnGlnGln
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/product= "Human rGAL-4 protein"
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/*tag= a
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New polynucleotide for producing active recombinant human and animal lysosomal enzymes in a plant expression system that can be used in enzyme replacement therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 TGGAAGGATGCAGGTTATGAGTACCTCTGCATTGATGACTGTTGGATGGCTCCCCAAAGA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human alpha-galactosidase derivatives and the nucleic acids encoding them. The polypeptides are used in a method for producing active recombinant human and animal lysosomal enzymes in a plant expression system. The enzymes can be used in enzyme replacement therapy for the therapeutic treatment of human and animal lysosomal diseases. This sequence represents DNA encoding a human alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MetGlnLeuArgAsnProGluLeuHisLeuGlyCysAlaLeuAlaLeuArgPheLeuAla
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(TURP/) TURPEN T H.
(KUMA/) KUMAGAI M H.
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  Homo sapiens.
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                                                                                                             GTAACTCAGATGGCCCTCTGGGCTATCATGGCTGCTCTTTATTCATGTCTAATGACCTC
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ThrCysAlaGlyPheProGlySerPheGlyTyrTyrAgpIleAspAlaGlnThrPheAla
                                                       AspTrpG1yValAspLeuLeuLysPheAspG1yCysTyrCysAspSerLeuG1uAsnLeu
                                                                         GACTGGGGAGTAGATCTGCTAAAATTTGATGGTTGTTACTGTGACAGTTTGGAAAATTTG
                                                                                                                                                                      SerCysGluTrpProLeuTyrMetTrpProPheGlnLysProAsnTyrThrGluIleArg
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                ACCTGCGCAGGCTTCCCTGGGGTTTTGGATACTACGACATTGATGCCCAGACCTTTGCT
                                                                                                                                                                                                   TCCTGTGAGTGGCCTCTTTATATGTGGCCCTTTCAAAAGCCCAATTATACAGAAATCCGA
                                                                                                                                                                                                                                                                                      SerIleLeuAspTrpThrSerPheAsnGlnGluArgIleValAspValAlaGlyProGly
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Galactosidase; GAL; gene therapy; ly
Fabry's disease; Gaucher's disease;
      rGAL- 4 (galactosidase) DNA
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961 CAGGACCCCTTGGGCAAGCAAGGTACCAGCTTAGACAGGGAGACAACTTTGAAGTGTGG 1020
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                                              AspTrpGlyValAspLeuLeuLysPheAspGlyCysTyrCysAspSerLeuGluAsnLeu
                                                                                                                                                                                                                       GGTTGGAATGACCCAGATATGTTAGTGATTGGCAACTTTGGCCTCAGCTGGAATCAGCAA
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                         GCTAATTATGTTCACAGCAAGGACTGAAGCTAGGGATTTATGCAGATGTTGGAAATAAA
                                                                                          GACTGGGGAGTAGATCTGCTAAAATTTGATGGTTGTTACTGTGACAGTTTGGAAAATTTG
                                                                                                             AlaAspGlyTyrLysHisMetSerLeuAlaLeuAsnArgThrGlyArgSerIleValTyr
                                                                                                                          GCAGATGGTTATAAGCACATGTCCTTGGCCCTGAATAGGACTGGCAGAAGCATTGTGTAC
                                                                                                                                               SerCysGluTrpProLeuTyrMetTrpProPheGlnLysProAsnTyrThrGluIleArg
                                                                                                                                                                              GlnTyrCysAsnHisTrpArgAsnPheAlaAspIleAspAspSerTrpLysSerIleLys
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GATTCAGAAGGCAGACTTCAGGCAGACCCTCAGCGCTTTCCTCATGGGATTCGCCAGCTA
                AlaAsnTyrValHisSerLysGlyLeuLysLeuGlyIleTyrAlaAspValGlyAsnLys
                                                                                                                                                                TCCTGTGAGTGGCCTCTTTATATGTGGCCCTTTCAAAAGCCCAATTATACAGAAATCCGA
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The invention relates to nucleotide encoding galactosidase (GAL). The invention is useful in gene therapy. The polynucleotides and polypeptides are useful in treating human and animal lysosomal storage diseases, e.g. Fabry's disease and Gaucher's diseases. The present sequence is human GAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New lysosomal enzymes, useful in treating human and animal lysosomal storage diseases, e.g. Fabry's disease and Gaucher's diseases.
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ERWIN R L.
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08-JUN-1989;
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16-JAN-1991;
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US-10-602-219-12 (1-421) x ADJ88272

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New alpha-galactosidase polypeptides, useful in producing recombinant lysosomal enzymes for the treatment of lysosomal storage diseases, such as Gaucher's disease, Niemann-Pick disease, Fabry disease and Tay-Sachs disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Galactosidase; Gal; lysosomal enzyme; enzyme replacement therapy;
lysosomal storage disease; Gaucher's disease; Niemann-Pick disease;
Fabry disease; Tay-Sachs disease; cardiovascular; nephrotrophic; human;
gene; ds.
GGACCTCGCTCTTATACCATCGCAGTTGCTTCCCTGGGTAAAGAGAGTGGCTGTAATCCT
                                                       AlaCysPhelleThrGlnLeuLeuProValLysArgLysLeuGlyPheTyrGluTrpThr
                                                                               GCCTGCTTCATCACACACCCCCCCCTGTGAAAAGGAAAGCTAGGGTTCTATGAATGGACT
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26-FEB-1988; 88US-00160771.

17-FEB-1989; 89US-00160244.

31-JUL-1992; 92US-0092733.

30-DEC-1992; 92US-0092733.

19-JAN-1994; 94US-00174414.

19-JAN-1994; 94US-00174414.

14-CTT-1994; 94US-00176414.

21-MAY-1999; 99US-0031603.

26-JUL-2000; 2000US-0056127.

26-JUL-2000; 2000US-0056127.
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KUMAGAI M H.
POGUE G P.
ERWIN R L.
GRILL L K.
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                                                                                                                                                                                                                                                  GATTCCTGCATCAGGGAAAGCTCTTCATGGAAATGGCAGAGCTCCATGGTCTCAGAAGGC
                                                                                                                                                                                                                                                                                                   TrpLyBAspAlaGlyTyrGluTyrLeuCysIleAspAspCysTrpMetAlaProGlnArg
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 MetGlnLeuArgAsnProGluLeuHisLeuGlyCysAlaLeuAlaLeuArgPheLeuAla
                            ATGCAGCTGAGGAACCCCAGAACTACATCTGGGCTGCGCGCTTGCGCTTCGCTTCCTGGCC
                                                                                                                                                    ThrMetGlyTrpLeuHisTrpGluArgPheMetCysAsnLeuAspCysGlnGluGluPro
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Lysosomal enzyme; glucocerebrosidase; GCB; GCR; alpha-galactosidase; enzyme replacement therapy; lysosomal storage disease, Gaucher's disease; Niemann-Pick disease; Fabry's disease; Tay-Sachs disease; Hurler's syndrome; Hurler-Scheie syndrome; nephrotropic; human; gene; ds.
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AGTATCTTGGACTGGACATCTTTTAACCAGGAGAGAATTGTTGATGTTGCTGGACCAGGG
                           GlyTrpAsnAspProAspMetLeuVallleGlyAsnPheGlyLeuSerTrpAsnGlnGln
                                                                                                                                               ArgHisIleSerProGlnAlaLysAlaLeuLeuGlnAspLysAspValIleAlaIleAsn
                                                                                                                                                                                                                                                                                   GCCTGCTTCATCATCACACACTCCTCCCTGTGAAAAGGAAGCTAGGGTTCTATGAATGGACT
                                                       GGTTGGAATGACCCAGATATGTTAGTGATTGGCAACTTTGGCCTCAGCTGGAATCAGCAA
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/transl_except= (pos:1. .6, aa:Gln)
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20-MAR-2002; 2002US-00103327.
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                                        The present invention relates to novel galactosidase (Gal) proteins such as rGAL-12, rGAL-12, rGAL-25 or rGAL-25.R. The methods and compositions of the present invention are useful for producing recombinant lysosomal enzymes for enzyme replacement therapy for treating human and animal lysosomal storage diseases such as Gaucher's disease, Niemann-pick disease, Pabry disease and Tay-Sachs disease. The present sequence is human wild type rGAL-4 DNA used in the exemplification of the invention.
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Matches:
Conservative:
Mismatches:
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             SEQ ID NO 7; 72pp; English.
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                                                                                                                      GlnTyrCysAsnHisTrpArgAsnPheAlaAspIleAspAspSerTrpLysSerIleLys 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 GlnAspProLeuGlyLysGlnGlyTyrGlnLeuArgGlnGlyAspAsnPheGluValTrp
                                                                                                                                                                                                            CAGTACTGCCAATCACTGCCGAAATTTTGCTGACATTGATGATTCCTGGAAAGTATAAAG
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                                                     SerCysGluTrpProLeuTyrMetTrpProPheGlnLysProAsnTyrThrGluIleArg
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                                                                                                                                                                                       The present invention relates to the production of human and animal lysosomal enzymes in plants by a transient plant expression system. The invention relates to glucocerebrosidase (GCB, GCR) and alphagalactosidase enzymes having a post-translational modification provided by the plant expression system. The invention is useful in enzyme replacement therapy for treating lysosomal storage diseases such as Gaucher's disease, Niemann-Pick disease, Fabry's disease and Tay-Sachs disease, Hurler's syndrome and Hurler-Scheie syndrome. The invention is treatment of lysosomal storage diseases and ray-Sachs treatment of lysosomal storage diseases and in industrial processes involving enzymatic substrate hydrolysis. The present sequence is the human alpha-galactosidase protein encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MetGlnLeuArgAsnProGluLeuHisLeuGlyCysAlaLeuAlaLeuArgPheLeuAla
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                                                                                        on comprising a lysosomal enzyme, useful for the treatment of lysosomal storage
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1278 BP; 325 A; 293 C; 333 G; 327 T; 0 U; 0 Other;
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                                                                                                                                                        Disclosure; SEQ ID NO 7; 88pp; English
     Kumagai MH
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diseases, such as Fabry's disease.
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                                                                                                                                                                                                                                                                                                                                                                                               lysosomal enzymes in plants by a transient plant expression system. The invention relates to glucocerebrosidase (GCB, GCR) and alpha-galactosidase (Gal) enzymes having a post-tranalational modification provided by the plant expression system. The invention is useful in enzyme replacement therapy for treating lysosomal storage diseases such as Gaucher's disease, Niemann-Pick disease, Fabry's disease, Tay-Sachs disease, Wirler's syndrome and Hurler-Scheis syndrome. The invention is also useful in researches for developing new approaches to medical treatment of lysosomal storage diseases and in industrial processes involving enzymatic substrate hydrolysis. The present sequence is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TrpLysAspAlaGlyTyrGluTyrLeuCysIleAspAspCysTrpMetAlaProGlnArg
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                                                                                                                                                                                                                                                                                    Diants to be utilized in enzyme replacement therapy or for the therapeutic treatment of human or animal lysosomal storage diseases, Gaucher's disease.
                                                                                                                                                                                                                                                                                                                                                                                       present invention relates to the production of human and animal
/*tag= b
/product= "Human alpha-galactosidase protein"
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                                      /note= "No start codon"
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                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 7; 88pp; English
                                                                                                                                                                                                                            Turpen TH, Kumagai MH;
                                                                                                                                                                                                 LARG-) LARGE SCALE BIOLOGY CORP.
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                                                                                                                                             26-JUL-2000; 2000US-00626127.
13-NOV-2001; 2001US-00993059.
20-MAR-2002; 2002US-00103327.
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P-PSDB; AEA27441, AEA27472.
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Best Local Similarity:
                                                                 US2005125859-A1
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                                                                                                                                                                                                                                                                                                                                                                                         Novel human alpha-galactosidase polypeptide useful for treating lysosomal storage diseases.
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                                                                     lysosomal enzyme; lysosomal storage disease; ds.
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/*tag= a
/product= "Human rGAL-8R
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                                                                    Human; alpha-galactosidase;
therapeutic; rGAL-8R; gene;
                        (first entry)
                                                                                                                                                                                                                                                                                                                                 Garger SJ, Turpen TH,
                                                                                                                                                                                                                                                                                 (GARG/) GARGER S J.
(TURP/) TURPEN T H.
(KUMA/) KUMAGAI M H.
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Best Local Similarity:
Query Match:
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                                               Human rGAL-8R DNA
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                        27-DEC-2002
                                                                                                       Homo sapiens
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AAD45224;
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                                                                                                                                               GlyProArgSerTyrThr11eAlaValAlaSerLeuGlyLysGlyValAlaCysAsnPro
                                    ThrMetGlyTrpLeuHisTrpGluArgPheMetCysAsnLeuAspCysGlnGluGluPro
                                                                                 AspSerCysIleSerGluLysLeuPheMetGluMetAlaGluLeuMetValSerGluGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotide for producing active recombinant human and animal lysosomal enzymes in a plant expression system that can be used in enzyme replacement therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 LeuValSerTrpAspIleProGlyAlaArgAlaLeuAspAsnGlyLeuAlaArgThrPro 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human alpha-galactosidase derivatives and the nucleic acids encoding them. The polypeptides are used in a method for producing active recombinant human and animal lysosomal enzymes in a plant expression system. The enzymes can be used in enzyme replacement therapy for the therapeutic treatment of human and animal lysosomal diseases. This sequence represents DNA encoding a human alpha-galactosidase derivative polypeptide of the invention.
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                                                                                                                                                                       alpha-galactosidase, rGAL-4; gene; ds; lysosomal enzyme; replacement therapy; lysosomal disease.
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                                                                                                                                                DNA.
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13-NOV-2001; 2001US-00993059
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P-PSDB; ADD84753.
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(TURP/) TURPEN T H.
(KUMA/) KUMAGAI M H.
                                                                          ADD84752 standard;
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Fabry's disease and Gaucher's diseases. The present sequence is human GAL.
DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New lysosomal enzymes, useful in treating human and animal lysosomal storage diseases, e.g. Fabry's disease and Gaucher's diseases.
                                                                                                                                                                                                                    Galactosidase; GAL; gene therapy; lysosomal storage disease;
Fabry's disease; Gaucher's disease; human; gene; ds.
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26-FEB-1988; 88US-00160771.
17-FEB-1989; 88US-00119279.
17-FEB-1989; 89US-00310881.
16-JAN-1989; 89US-00347637.
22-OCT-1990; 90US-0060244.
16-JAN-1991; 91US-0061617.
16-JAN-1991; 91US-00737899.
11-JUL-1991; 91US-00737899.
21-JUL-1991; 91US-00737899.
21-JUL-1991; 91US-00737899.
21-JUL-1991; 91US-00176414.
19-JAN-1994; 94US-001164237.
21-MAY-1994; 94US-001164237.
21-MAY-1999; 99US-00316572.
26-JUL-2000; 2000US-00626127.
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ERWIN R L.
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